GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 19, 2005, 03:00:42 ; Search time 31 Seconds
(without alignments)
3236.398 Million cell updates/sec

Title: US-10-066-521-6
Perfect score: 7074
Sequence: 1 MEGDKSLTFSSYGLQWCLYE.....DDHSGVSWSLGAAGLEGLVS 1344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	945.5	13.4	1454	4	US-09-388-221B-10	Sequence 10, Appl
2	945.5	13.4	1473	4	US-09-388-221B-2	Sequence 2, Appli
3	938.5	13.3	1399	4	US-09-388-221B-4	Sequence 4, Appli
4	938.5	13.3	1424	4	US-09-388-221B-12	Sequence 12, Appl
5	938.5	13.3	1443	4	US-09-388-221B-6	Sequence 6, Appli
6	630.5	8.9	456	2	US-08-910-731-4	Sequence 4, Appli
7	630.5	8.9	456	2	US-08-795-395-4	Sequence 4, Appli
8	621	8.8	456	2	US-08-910-731-2	Sequence 2, Appli
9	621	8.8	456	2	US-08-795-395-2	Sequence 2, Appli
10	612	8.7	456	2	US-08-910-731-8	Sequence 8, Appli
11	607.5	8.6	461	2	US-08-910-731-6	Sequence 6, Appli
12	374.5	5.3	953	3	US-09-245-281-43	Sequence 43, Appl
13	374.5	5.3	953	4	US-09-207-359B-43	Sequence 43, Appl
14	374.5	5.3	953	4	US-09-340-620A-43	Sequence 43, Appl
15	374.5	5.3	953	4	US-09-865-364-43	Sequence 43, Appl
16	364	5.1	1013	4	US-10-014-269-3	Sequence 3, Appli
17	364	5.1	1040	4	US-10-014-269-2	Sequence 2, Appli
18	364	5.1	1043	4	US-09-949-016-9080	Sequence 9080, Ap
19	363	5.1	1040	4	US-10-014-269-4	Sequence 4, Appli
20	356.5	5.0	209	4	US-09-388-221B-19	Sequence 19, Appl
21	347	4.9	953	3	US-09-099-041A-8	Sequence 8, Appli
22	347	4.9	953	3	US-09-245-281-8	Sequence 8, Appli
23	347	4.9	953	4	US-09-207-359B-8	Sequence 8, Appli
24	347	4.9	953	4	US-09-340-620A-8	Sequence 8, Appli
25	347	4.9	953	4	US-09-865-364-8	Sequence 8, Appli
26	345	4.9	1007	4	US-10-014-269-34	Sequence 34, Appl
27	324.5	4.6	966	4	US-09-207-359B-47	Sequence 47, Appl
28	324.5	4.6	966	4	US-09-865-364-47	Sequence 47, Appl
29	306.5	4.3	830	4	US-09-064-199-19	Sequence 19, Appl
30	306.5	4.3	1106	4	US-09-064-199-17	Sequence 17, Appl
31	306.5	4.3	1130	2	US-08-519-547A-6	Sequence 6, Appli
32	306.5	4.3	1130	4	US-09-064-199-18	Sequence 18, Appl
33	306.5	4.3	1207	4	US-09-064-199-16	Sequence 16, Appl
34	213	3.0	483	4	US-09-904-615-154	Sequence 154, App
35	163	2.3	305	4	US-10-014-269-7	Sequence 7, Appli
36	160	2.3	1240	3	US-08-930-996A-4	Sequence 4, Appli
37	153.5	2.2	490	3	US-09-099-041A-26	Sequence 26, Appl
38	153.5	2.2	490	3	US-09-245-281-26	Sequence 26, Appl
39	153.5	2.2	490	4	US-09-207-359B-26	Sequence 26, Appl
40	153.5	2.2	490	4	US-09-340-620A-26	Sequence 26, Appl
41	153.5	2.2	490	4	US-09-865-364-26	Sequence 26, Appl
42	149	2.1	509	3	US-08-809-999D-17	Sequence 17, Appl
43	149	2.1	509	3	US-09-069-637-17	Sequence 17, Appl
44	149	2.1	509	3	US-09-322-360-17	Sequence 17, Appl
45	149	2.1	509	3	US-09-131-831B-17	GENERAL INFORMA

ALIGNMENTS

RESULT 1
US-09-388-221B-10
; Sequence 10, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Construct
US-09-388-221B-10

Query Match 13.4%; Score 945.5; DB 4; Length 1454;
Best Local Similarity 24.8%; Pred. No. 5.7e-83;
Matches 294; Conservative 162; Mismatches 339; Indels 389; Gaps 30;

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Qy          11 SYGLQWCLYE-LDKEEFQTFKELLKKKS-SESTTCSIPQFEIENANVECLALLLHEYYGA 68
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Db           5 AWGRLACYLEFLKKEELKEFQLLLANKAHSRSSSGETPAQPEKTSGMEVASYLVAQ-YGE 63

Qy          69 SLAWATSISIFENMNLRTLSEKARDD---------------------------------- 94
                 ||  ::  :| | ||:|  :|::
Db          64 QRAWDLALHTWEQMGLRSLCAQAQEGAGHSPSFPYSPSEPHLGSPSQPTSTAVLMPWIHE 123

Qy          95 ------------------------MKKISQAM---------------------------- 102
                                        ::|| ::
Db         124 LPAGCTQGSERRVLRQLPDTSGRRWREISASLLYQALPSSPDHESPSQESPNAPTSTAVL 183

Qy         103 --------------EQEGA--------------TAAETEEQEISQAMEQEGATAAETEEQ 134
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Db         184 GSWGSPPQPSLAPREQEAPGTQWPLDETSGIYYTEIRERERERKSEKGRPPWAAVVGTPPQ 243

Qy         135 GHGG----------------DTWDYKSHVMT-KF------------AEEEDVRRSFENT 164
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Db         244 AHTSLQPHHHPWEPSVRESLCSTWPWKNEDFNQKFTQLLLLQRPHPRSQDPLVKRS---- 299

Qy         165 AADWP-----------EMQTLAG-AFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWA 212
                  ||           |:: | |   |:      || |:| | :|||| |||::   |
Db         300 ---WPDYVEENRGHLIEIRDLFGPGLDTQ----EPRIVILQGAAGIGKSTLARQVKEAWG 352

Qy         213 QGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGF 272
               :| ||   | :||:   ||: : |  |: | | ::   : ||: :|:||||||||:||
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Db        353 RGQLYGDRFQHVFYFSCRELAQSKVVSLAELIGKDGTATPAPIRQILSRPERLLFILDGV 412

Qy        273 DDLGSVLNN-DTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVS 331
              |: | ||    ::|| |:: ||   |: ||| | :|||:  ::| |    : |   :
Db        413 DEPGWVLQEPSSELCLHWSQPQPADALLGSLLGKTILPEASFLITARTTALQNLIPSLEQ 472

Qy        332 PRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQL 391
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Db        473 ARWVEVLGFSESSRKEYFYRYFTDERQAIRAFRLVKSNKELWALCLVPWVSWLACTCLMQ 532

Qy        392 QDVVGESVAPFNQTLTG--LHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWN 449
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Db        533 QMKRKEKLTLTSKTTTTLCLHYLAQALQAQPLG-----------PQLRDLCSLAAEGIWQ 581

Qy        450 RKSVFDGDDLMVQGLGESELRALFHMNIL----LPDSHCEEYYTFFHLSLQDFCAALYYV 505
              :|::|  |||   ||  : :     | ||    :| |     |:| ||  |:| ||: ||
Db        582 KKTLFSPDDLRKHGLDGAIISTFLKMGILQEHPIPLS-----YSFIHLCFQEFFAAMSYV 636

Qy        506 LEGLE--IEPALCPLYVEKTKRSMELKQAGFHIHSLW---MKRFLFGLVSEDVRRPLEVL 560
              ||  :   : : | : :|||  :       : || |:     ||| ||:|::  | :| :
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Qy        561 LGCPVPLGVKQKLLHWVSLLG--QQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEV 618
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Db        690 FHCRLSQG--RNLMQWVPSLQLLLQPH------SLESLHCLYETRNKTFLTQVMAHFEEM 741

Qy        619 WLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQW 678
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Db        742 GMCVETDMELLVCTFCIKFSRHVKKLQL-IEG---RQHRSTWSPTMVVLFRWVPVTDAYW 797

Qy        679 EDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLW 738
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Db        798 ------------------------------------------------------QILF 801

Qy        739 RIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQIL 798
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Db        802 SVLKVTRNLKELDLSGNSLSHSAVKSLCKTLRRPRCLLETLR----------------- 843

Qy        799 TTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSN 858
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Db        844 ----------LAG--------------------------CGLTAEDCKDLAFGLRAN 864

Qy        859 RSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWL 918
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Db        865 QT-------------------------------------------------------L 867

Qy        919 THLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSL 978
              | | || | : | | | ||: :|:||| || |:|| | ||: ||: |: |:| |  || |
Db        868 TELDLSFNVLTDAGAKHLCQRLRQPSCKLQRLQLVSCGLTSDCCQDLASVLSASPSLKEL 927

Qy        979 DLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEAL 1022
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Db        928 DLQQNNLDDVGVRLLCEGLRHPACKLIRLGLDQTTLSDEMRQEL 971
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RESULT 2
US-09-388-221B-2
; Sequence 2, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-388-221B-2

Query Match 13.4%; Score 945.5; DB 4; Length 1473;
Best Local Similarity 24.8%; Pred. No. 5.8e-83;
Matches 294; Conservative 162; Mismatches 339; Indels 389; Gaps 30;

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Qy         11 SYGLQWCLYE-LDKEEFQTFKELLKKKS-SESTTCSIPQFEIENANVECLALLLHEYYGA 68
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Db          5 AWGRLACYLEFLKKEELKEFQLLLANKAHSRSSSGETPAQPEKTSGMEVASYLVAQ-YGE 63

Qy         69 SLAWATSISIFENMNLRTLSEKARDD-------------------------------- 94
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Db         64 QRAWDLALHTWEQMGLRSLCAQAQEGAGHSPSFPYSPSEPHLGSPSQPTSTAVLMPWIHE 123

Qy         95 ------------------------MKKISQAM---------------------------- 102
                                       ::|| ::
Db        124 LPAGCTQGSERRVLRQLPDTSGRRWREISASLLYQALPSSPDHESPSQESPNAPTSTAVL 183

Qy        103 --------------EQEGA--------------TAAETEEQEISQAMEQEGATAAETEEQ 134
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Db        184 GSWGSPPQPSLAPREQEAPGTQWPLDETSGIYYTEIRERERERKSEKGRPPWAAVVGTPPQ 243

Qy        135 GHGG-----------------DTWDYKSHVMT-KF------------AEEEDVRRSFENT 164
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Db        244 AHTSLQPHHHPWEPSVRESLCSTWPWKNEDFNQKFTQLLLLQRPHPRSQDPLVKRS---- 299

Qy        165 AADWP-----------EMQTLAG-AFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWA 212
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Db        300 ---WPDYVEENRGHLIEIRDLFGPGLDTQ----EPRIVILQGAAGIGKSTLARQVKEAWG 352

Qy        213 QGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGF 272
              :| ||   | :||:   ||: : |  |: | | ::   : ||: :|:|||||||||:||
Db        353 RGQLYGDRFQHVFYFSCRELAQSKVVSLAELIGKDGTATPAPIRQILSRPERLLFILDGV 412

Qy        273 DDLGSVLNN-DTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVS 331
              |: | ||    ::||  |:: ||   |: ||| | :|||:  ::| |    : |   :
Db        413 DEPGWVLQEPSSELCLHWSQPQPADALLGSLLGKTILPEASFLITARTTALQNLIPSLEQ 472

Qy        332 PRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQL 391
              |:: | | |   |           | |  :  | : :|:||   | || |  | |  |
Db        473 ARWVEVLGFSESSRKEYFYRYFTDERQAIRAFRLVKSNKELWALCLVPWVSWLACTCLMQ 532

Qy        392 QDVVGESVAPFNQTLTG--LHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWN 449
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Db        533 QMKRKEKLTLTSKTTTTLCLHYLAQALQAQPLG-----------PQLRDLCSLAAEGIWQ 581

Qy        450 RKSVFDGDDLMVQGLGESELRALFHMNIL----LPDSHCEEYYTFFHLSLQDFCAALYYV 505
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Db        582 KKTLFSPDDLRKHGLDGAIISTFLKMGILQEHPIPLS-----YSFIHLCFQEFFAAMSYV 636

Qy        506 LEGLE--IEPALCPLYVEKTKRSMELKQAGFHIHSLW---MKRFLFGLVSEDVRRPLEVL 560
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Db        637 LEDEKGRGKHSNCIIDLEKTLEA-------YGIHGLFGASTTRFLLGLLSDEGEREMENI 689

Qy        561 LGCPVPLGVKQKLLHWVSLLG--QQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEV 618
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Db        690 FHCRLSQG--RNLMQWVPSLQLLLQPH------SLESLHCLYETRNKTFLTQVMAHFEEM 741

Qy        619 WLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQW 678
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Db        742 GMCVETDMELLVCTFCIKFSRHVKKLQL-IEG---RQHRSTWSPTMVVLFRWVPVTDAYW 797

Qy        679 EDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLW 738
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Db        798 ------------------------------------------------------QILF 801

Qy        739 RIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQIL 798
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Db        802 SVLKVTRNLKELDLSGNSLSHSAVKSLCKTLRRPRCLLETLR----------------- 843

Qy        799 TTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSN 858
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Db        844 ----------LAG--------------------------CGLTAEDCKDLAFGLRAN 864

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Db        865 QT-----------------------------------------------------L 867

Qy        919 THLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSL 978
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Db        868 TELDLSFNVLTDAGAKHLCQRLRQPSCKLQRLQLVSCGLTSDCCQDLASVLSASPSLKEL 927

Qy        979 DLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEAL 1022
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Db        928 DLQQNNLDDVGVRLLCEGLRHPACKLIRLGLDQTTLSDEMRQEL 971


RESULT 3
US-09-388-221B-4
; Sequence 4, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 1399
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-388-221B-4

  Query Match           13.3%;  Score 938.5;  DB 4;  Length 1399;
  Best Local Similarity   24.9%;  Pred. No. 2.6e-82;
  Matches  291;  Conservative  159;  Mismatches  331;  Indels  389;  Gaps   30;

Qy         11 SYGLQWCLYE-LDKEEFQTFKELLKKKS-SESTTCSIPQFEIENANVECLALLLHEYYGA 68
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Db          5 AWGRLACYLEFLKKEELKEFQLLLANKAHSRSSSGETPAQPEKTSGMEVASYLVAQ-YGE 63

Qy         69 SLAWATSISIFENMNLRTLSEKARDD---------------------------------- 94
                ||  ::  :| | ||:|  :|::
Db         64 QRAWDLALHTWEQMGLRSLCAQAQEGAGHSPSFPYSPSEPHLGSPSQPTSTAVLMPWIHE 123

Qy         95 ------------------------MKKISQAM---------------------------- 102
                                       ::|| ::
Db        124 LPAGCTQGSERRVLRQLPDTSGRRWREISASLLYQALPSSPDHESPSQESPNAPTSTAVL 183

Qy        103 --------------EQEGA--------------TAAETEEQEISQAMEQEGATAAETEEQ 134
                           |||                |     |:| |:      |    | |
Db        184 GSWGSPPQPSLAPREQEAPGTQWPLDETSGIYYTEIRERE-REKSEKGRPPWAAVVGTPPQ 243

Qy        135 GHGG-----------------DTWDYKSHVMT-KF------------AEEEDVRRSFENT 164
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Qy        165 AADWP----------EMQTLAG-AFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWA 212
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Db        300 ---WPDYVEENRGHLIEIRDLFGPGLDTQ----EPRIVILQGAAGIGKSTLARQVKEAWG 352

Qy        213 QGGLYQGMPSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGF 272
              :| ||   | :||:   ||: : |  |: | | ::   : ||: :|:|||||||||:||
Db        353 RGQLYGDRFQHVFYFSCRELAQSKVVSLAELIGKDGTATPAPIRQILSRPERLLFILDGV 412

Qy        273 DDLGSVLNN-DTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVS 331
              |: | ||    ::||  |:: ||   |: ||| | :|||:  ::| |    : |   :
Db        413 DEPGWVLQEPSSELCLHWSQPQPADALLGSLLGKTILPEASFLITARTTALQNLIPSLEQ 472

Qy        332 PRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQL 391
              |:: | | |      |  |  :  | : :|:||   | || |  | |   |
Db        473 ARWVEVLGFSESSRKEYFYRYFTDERQAIRAFRLVKSNKELWALCLVPWVSWLACTCLMQ 532

Qy        392 QDVVGESVAPFNQTLTG--LHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWN 449
              |    | :   ::| |   ||       | | |            |:  | :| ||:|
Db        533 QMKRKEKLTLTSKTTTTLCLHYLAQALQAQPLG----------PQLRDLCSLAAEGIWQ 581
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Db        582 KKTLFSPDDLRKHGLDGAIISTFLKMGILQEHPIPLS-----YSFIHLCFQEFFAAMSYV 636

Qy        506 LEGLE--IEPALCPLYVEKTKRSMELKQAGFHIHSLW---MKRFLFGLVSEDVRRPLEVL 560
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Qy        561 LGCPVPLGVKQKLLHWVSLLG--QQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEV 618
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Qy        619 WLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQW 678
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Db        742 GMCVETDMELLVCTFCIKFSRHVKKLQL-IEG---RQHRSTWSPTMVVLFRWVPVTDAYW 797

Qy        679 EDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLW 738
                                                                    | |:
Db        798 ---------------------------------------------------QILF 801

Qy        739 RIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQIL 798
              ::   |||: |:| |  |    |:  |: |: |:||||:||
Db        802 SVLKVTRNLKELDLSGNSLSHSAVKSLCKTLRRPRCLLETLR---------------- 843

Qy        799 TTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSN 858
                        |||                          ||:||  |: ||  | :|
Db        844 ----------LAG---------------------------CGLTAEDCKDLAFGLRAN 864

Qy        859 RSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWL 918
              ::                                                       |
Db        865 QT-----------------------------------------------------L 867

Qy        919 THLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSL 978
              | | || | : | | | ||: :|:||| || |:|| | ||: ||: |: |:| |  || |
Db        868 TELDLSFNVLTDAGAKHLCQRLRQPSCKLQRLQLVSCGLTSDCCQDLASVLSASPSLKEL 927

Qy        979 DLTDNALGDGGVAALCEGLKQKNSVLTRLG 1008
              ||  | | | ||  |||||:     | |||
Db        928 DLQQNNLDDVGVRLLCEGLRHPACKLIRLG 957


RESULT 4
US-09-388-221B-12
; Sequence 12, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 1424
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic Construct
US-09-388-221B-12

  Query Match           13.3%;  Score 938.5;  DB 4;  Length 1424;
  Best Local Similarity   24.9%;  Pred. No. 2.7e-82;
  Matches  291;  Conservative  159;  Mismatches  331;  Indels  389;  Gaps   30;

Qy         11 SYGLQWCLYE-LDKEEFQTFKELLKKKS-SESTTCSIPQFEIENANVECLALLLHEYYGA 68
              ::|   |  | | ||| : |: ||  |: | |::   |    : : :|  : |: : ||
Db          5 AWGRLACYLEFLKKEELKEFQLLLANKAHSRSSSGETPAQPEKTSGMEVASYLVAQ-YGE 63

Qy         69 SLAWATSISIFENMNLRTLSEKARDD---------------------------------- 94
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Db         64 QRAWDLALHTWEQMGLRSLCAQAQEGAGHSPSFPYSPSEPHLGSPSQPTSTAVLMPWIHE 123
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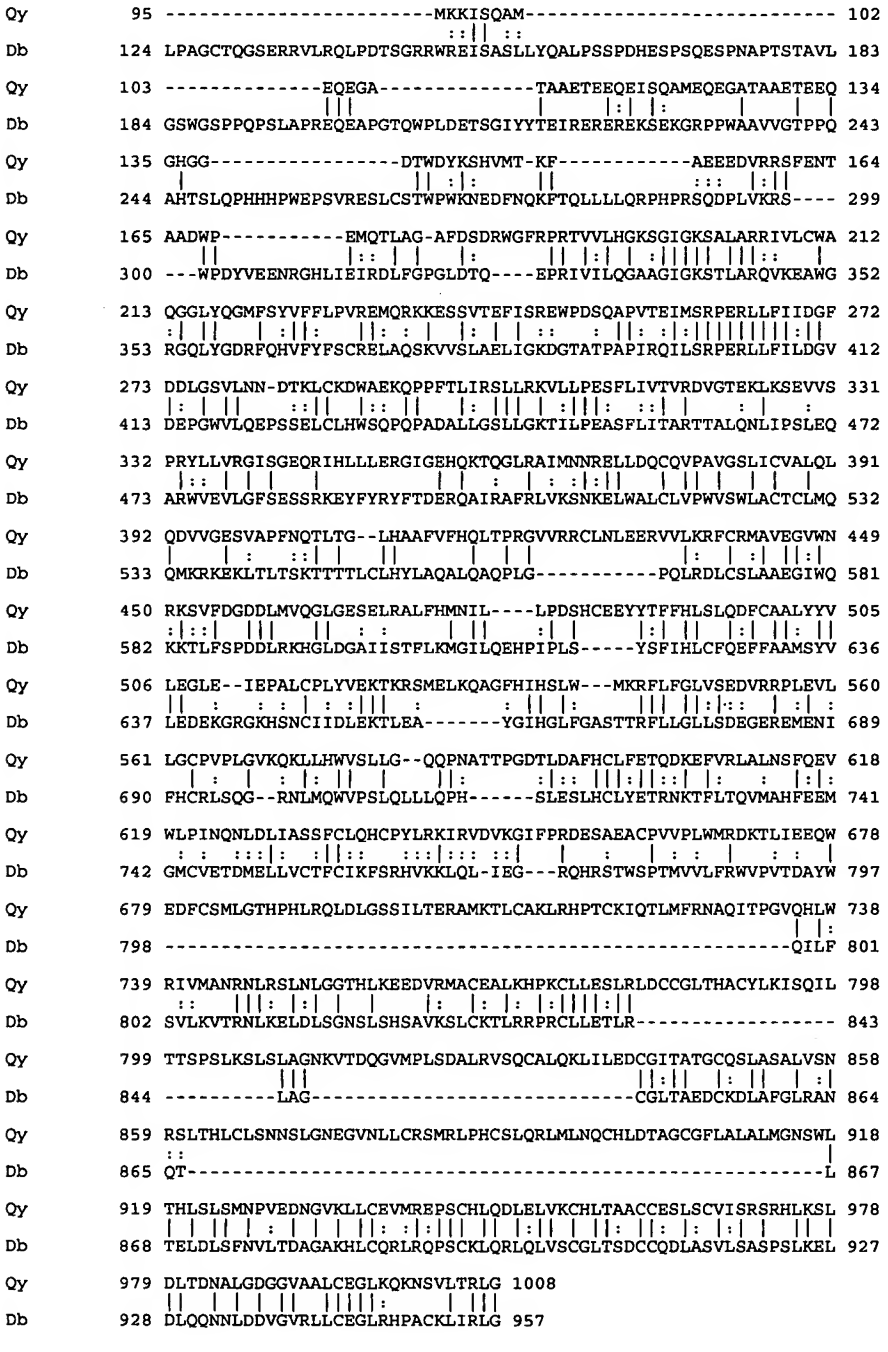
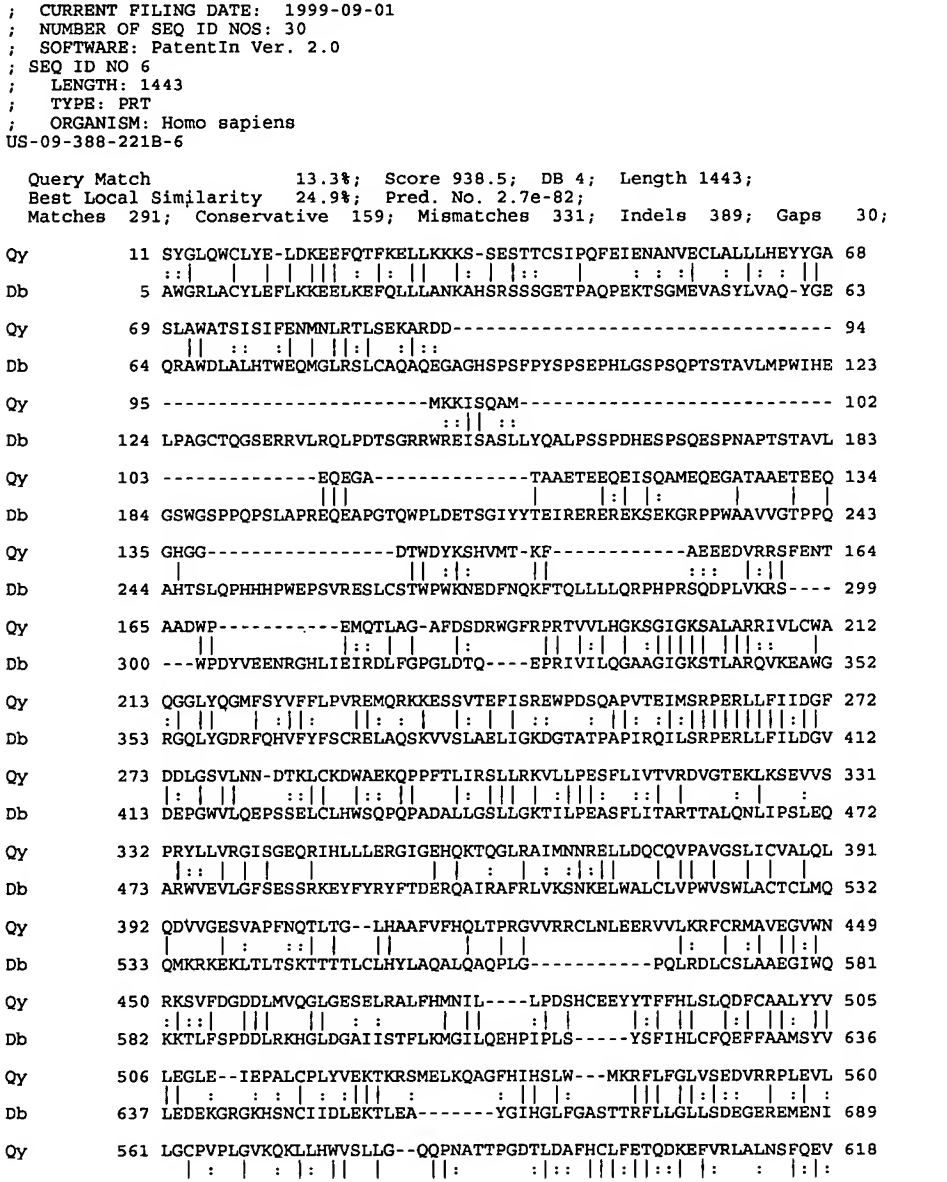


RESULT 5
US-09-388-221B-6
; Sequence 6, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-388-221B-6

Query Match 13.3%; Score 938.5; DB 4; Length 1443;
Best Local Similarity 24.9%; Pred. No. 2.7e-82;
Matches 291; Conservative 159; Mismatches 331; Indels 389; Gaps 30;



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Db        690 FHCRLSQG--RNLMQWVPSLQLLLQPH------SLESLHCLYETRNKTFLTQVMAHFEEM 741

Qy        619 WLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQW 678

Db        742 GMCVETDMELLVCTFCIKFSRHVKKLQL-IEG---RQHRSTWSPTMVVLFRWVPVTDAYW 797

Qy        679 EDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLW 738

Db        798 ------------------------------------------------------QILF 801

Qy        739 RIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQIL 798

Db        802 SVLKVTRNLKELDLSGNSLSHSAVKSLCKTLRRPRCLLETLR------------------ 843

Qy        799 TTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSN 858

Db        844 ----------LAG----------------------------CGLTAEDCKDLAFGLRAN 864

Qy        859 RSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWL 918

Db        865 QT-------------------------------------------------------L 867

Qy        919 THLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSL 978

Db        868 TELDLSFNVLTDAGAKHLCQRLRQPSCKLQRLQLVSCGLTSDCCQDLASVLSASPSLKEL 927

Qy        979 DLTDNALGDGGVAALCEGLKQKNSVLTRLG 1008

Db        928 DLQQNNLDDVGVRLLCEGLRHPACKLIRLG 957


RESULT 6
US-08-910-731-4
; Sequence 4, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  456 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-910-731-4

  Query Match             8.9%;  Score 630.5;  DB 2;  Length 456;
  Best Local Similarity   34.0%;  Pred. No. 8.5e-53;
  Matches  147;  Conservative   75;  Mismatches  201;  Indels    9;  Gaps    3;

Qy        659 EACPVVPLW----MRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLR 714

Db         17 ELLPLIQQYQVVRLDDCGLTEVRCKDIRSAIQANPALTELSLRTNELGDAGVGLVLQGLQ 76

Qy        715 HPTCKIQTLMFRNAQIT-PGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPK 773

Db         77 NPTCKIQKLSLQNCSLTEAGCGVLPDVLRSLSTLRELHLNDNPLGDEGLKLLCEGLRDPQ 136

Qy        774 CLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCAL 833

Db        137 CRLEKLQLEYCNLTATSCEPLASVLRVKPDFKELVLSNNDFHEAGIHTLCQGLKDSACQL 196

Qy        834 QKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRL 893

Db        197 ESLKLENCGITSANCKDLCDVVASKASLQELDLGSNKLGNTGIAALCSGLLLPSCRLRTL 256

Qy        894 MLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELV 953

Db        257 WLWDCDVTAEGCKDLCRVLRAKQSLKELSLAGNELKDEGAQLLCESLLEPGCQLESLWVK 316

Qy        954 KCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACG 1013

Db        317 TCSLTAASCPHFCSVLTKNSSLFELQMSSNPLGDSGVVELCKALGYPDTVLRVLWLGDCD 376

Qy       1014 LTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGL----WKW 1069

Db        377 VTDSGCSSLATVLLANRSLRELDLSNNCMGDNGVLQLLESLKQPSCILQQLVLYDIYWTD 436

Qy       1070 QYPVQIRKLLEE 1081

Db        437 EVEDQLRALEEE 448


RESULT 7
US-08-795-395-4
; Sequence 4, Application US/08795395
; Patent No. 5965399
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Cloning and Expression of Rat Liver and
;    TITLE OF INVENTION:  Porcine Liver Ribonuclease Inhibitor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,395
;      FILING DATE:  04-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  456 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-395-4

  Query Match             8.9%;  Score 630.5;  DB 2;  Length 456;
  Best Local Similarity   34.0%;  Pred. No. 8.5e-53;
  Matches  147;  Conservative   75;  Mismatches  201;  Indels    9;  Gaps    3;

Qy        659 EACPVVPLW----MRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLR 714
              |  |::  :    : |  | | : :|  | :  :| | :| | :: | :  :  :   |:
Db         17 ELLPLIQQYQVVRLDDCGLTEVRCKDIRSAIQANPALTELSLRTNELGDAGVGLVLQGLQ 76

Qy        715 HPTCKIQTLMFRNAQIT-PGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPK 773
              :|||||  |  :|  :|  |  |  :: :  || |:|    | :| ::: || |: |:
Db         77 NPTCKIQKLSLQNCSLTEAGCGVLPDVLRSLSTLRELHLNDNPLGDEGLKLLCEGLRDPQ 136

Qy        774 CLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCAL 833
              | || |:|: | ||      :: :|   |  | | |: |   : |:  |   |: | | |
Db        137 CRLEKLQLEYCNLTATSCEPLASVLRVKPDFKELVLSNNDFHEAGIHTLCQGLKDSACQL 196

Qy        834 QKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRL 893
              : | ||:||||:  |: |   : |  ||  | | :| ||| |:  ||  : || | |: |
Db        197 ESLKLENCGITSANCKDLCDVVASKASLQELDLGSNKLGNTGIAALCSGLLLPSCRLRTL 256

Qy        894 MLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELV 953
             |  | :   ||  |  |    |  |||: | ::| | :|||| : || | |: | :
Db        257 WLWDCDVTAEGCKDLCRVLRAKQSLKELSLAGNELKDEGAQLLCESLLEPGCQLESLWVK 316

Qy        954 KCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACG 1013
              | |||| |     |:::  |  | :: | ||| ||  ||: |  ::|| | |  |
Db        317 TCSLTAASCPHFCSVLTKNSSLFELQMSSNPLGDSGVVELCKALGYPDTVLRVLWLGDCD 376

Qy       1014 LTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGL----WKW 1069
              :|   | :|:  |  || |  |:|  |      |:::|  :   |:  || : |    |
Db        377 VTDSGCSSLATVLLANRSLRELDLSNNCMGDNGVLQLLESLKQPSCILQQLVLYDIYWTD 436

Qy       1070 QYPVQIRKLLEE 1081
              .  :   |:| | ||
Db        437 EVEDQLRALEEE 448


RESULT 8
US-08-910-731-2
; Sequence 2, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  456 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-910-731-2

  Query Match             8.8%;  Score 621;  DB 2;  Length 456;
  Best Local Similarity   31.9%;  Pred. No. 7.4e-52;
  Matches  151;  Conservative   86;  Mismatches  210;  Indels   26;  Gaps    5;

Qy        625 NLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLW----MRDKTLIEEQWED 680
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Db          2 NLDI--------HCEQLSDAR-----------WTELLPLLQQYEVVRLDDCGLTEEHCKD 42

Qy        681 FCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQIT-PGVQHLWR 739
              | |  :| | :| | :: | :  :  :   |: ||||||  |  :|  :|  |   |
Db         43 IGSALRANPSLTELCLRTNELGDAGVHLVLQGLQSPTCKIQKLSLQNCSLTEAGCGVLPS 102

Qy        740 IVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILT 799
              : :   || |:|    | :  :|: || |  |:| || |:|: | || |    :: :|
Db        103 TLRSLPTLRELHLSDNPLGDAGLRLLCEGLLDPQCHLEKLQLEYCRLTAASCEPLASVLR 162

Qy        800 TSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNR 859
              : :|| |::: | : : |    |   | | |: | ||:||:|    |: |   : |
Db        163 ATRALKELTVSNNDIGEAGARVLGQGLADSACQLETLRLENCGLTPANCKDLCGIVASQA 222

Qy        860 SLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLT 919
              ||  | | :| ||: |:  ||  :  |   |: | | :| :  :|| |   |      |
Db        223 SLRELDLGSNGLGDAGIAELCPGLLSPASRLKTLWLWECDITASGCRDLCRVLQAKETLK 282

Qy        920 HLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLD 979
              |||: | : | | :|||| : :| | |: | :  | ||||||: :| ::::::||  |
Db        283 ELSLAGNKLGDEGARLLCESLLQPGCQLESLWVKSCSLTAACCQHVSLMLTQNKHLLELQ 342

Qy        980 LTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQ 1039
              |: | ||| |:  ||: | |  :| | | | :|:  | :|:  |  || |  |:|
Db        343 LSSNKLGDSGIQELCQALSQPGTTLRVLCLGDCEVTNSGCSSLASLLLANRSLRELDLSN 402

Qy       1040 NNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKP--RVV 1090
              |      |:::|  :    |  |: : |:   :  ::   |: ::  ||  ||:
Db        403 NCVGDPGVLQLLGSLEQPGCALEQLVLYDTYWTEEVEDRLQALEGSKPGLRVI 455


RESULT 9
US-08-795-395-2
; Sequence 2, Application US/08795395
; Patent No. 5965399
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Cloning and Expression of Rat Liver and
```

```
;    TITLE OF INVENTION:  Porcine Liver Ribonuclease Inhibitor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,395
;      FILING DATE:  04-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  456 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-795-395-2

  Query Match             8.8%;  Score 621;  DB 2;  Length 456;
  Best Local Similarity   31.9%;  Pred. No. 7.4e-52;
  Matches  151;  Conservative   86;  Mismatches  210;  Indels   26;  Gaps    5;

Qy        625 NLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLW----MRDKTLIEEQWED 680
              |||:          ||  |    |              |  |::  :    : |  | ||  :|
Db          2 NLDI--------HCEQLSDAR----------WTELLPLLQQYEVVRLDDCGLTEEHCKD 42

Qy        681 FCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQIT-PGVQHLWR 739
                | |  :| | :| | :: | :  :  :   |: |||||| |  :|  :|  |   |
Db         43 IGSALRANPSLTELCLRTNELGDAGVHLVLQGLQSPTCKIQKLSLQNCSLTEAGCGVLPS 102

Qy        740 IVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILT 799
              : :   || |:|    | :  :|: || |  |:| || |:|: | || |    :: :|
Db        103 TLRSLPTLRELHLSDNPLGDAGLRLLCEGLLDPQCHLEKLQLEYCRLTAASCEPLASVLR 162

Qy        800 TSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNR 859
              : :|| |::: | : : |   |   |  | | |: | ||:||:|   |: |   : |
Db        163 ATRALKELTVSNNDIGEAGARVLGQGLADSACQLETLRLENCGLTPANCKDLCGIVASQA 222

Qy        860 SLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLT 919
              ||  | | :| ||: |:  ||  :  |   |: | | :| :  :||  |   |      |
Db        223 SLRELDLGSNGLGDAGIAELCPGLLSPASRLKTLWLWECDITASGCRDLCRVLQAKETLK 282

Qy        920 HLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLD 979
              |||: | : | | :|||| : :| | |: | :  | ||||||: :| ::::::||  |
Db        283 ELSLAGNKLGDEGARLLCESLLQPGCQLESLWVKSCSLTAACCQHVSLMLTQNKHLLELQ 342

Qy        980 LTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQ 1039
              |: | ||| |:  ||: | |  : |  | | |:|:  | :|:  |  || |  |:|
Db        343 LSSNKLGDSGIQELCQALSQPGTTLRVLCLGDCEVTNSGCSSLASLLLANRSLRELDLSN 402

Qy       1040 NNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKP--RVV 1090
              |     |:::|  :   |   |: : |:  :  ::   |: ::  ||  ||:
Db        403 NCVGDPGVLQLLGSLEQPGCALEQLVLYDTYWTEEVEDRLQALEGSKPGLRVI 455

RESULT 10
US-08-910-731-8
; Sequence 8, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  456 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  peptide
US-08-910-731-8

  Query Match             8.7%;  Score 612;  DB 2;  Length 456;
  Best Local Similarity   32.1%;  Pred. No. 5.7e-51;
  Matches  152;  Conservative   81;  Mismatches  214;  Indels   26;  Gaps    5;

Qy        625 NLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLW----MRDKTLIEEQWED 680
              |||:          ||  |    |              |  |::  :    : |  | ||  :|
Db          2 NLDI--------HCEQLSDAR----------WTELLPLLQQYEVVRLDDCGLTEEHCKD 42

Qy        681 FCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQIT-PGVQHLWR 739
                | |  :| | :| | :: | :  :  :   |: |||||| |  :|  :|  |   |
Db         43 IGSALRANPSLTELCLRTNELGDAGVHLVLQGLQSPTCKIQKLSLQNCSLTEAGCGVLPS 102

Qy        740 IVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILT 799
              : :   || |:|    | :  :|: || |  |:| || |:|: | || |    :: :|
Db        103 TLRSLPTLRELHLSDNPLGDAGLRLLCEGLLDPQCHLEKLQLEYCRLTAASCEPLASVLR 162

Qy        800 TSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNR 859
              : :|| |::: | : : |   |   |  | | |: | ||:||:|   |: |   : |
Db        163 ATRALKELTVSNNDIGEAGARVLGQGLADSACQLETLRLENCGLTPANCKDLCGIVASQA 222

Qy        860 SLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLT 919
              ||  | | :| ||: |:  ||  :  |   |: | : :|  :   |||  |   |      |
Db        223 SLRELALGSNKLGDVGMAELCPGLLHPSSRLRTLWIWECGITAKGCGDLCRVLRAKESLK 282
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Qy        920 HLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLD 979
              |||: | : | | :|||| : || | |: | :  |  |||||   | |::::| |  |
Db        283 ELSLAGNELGDEGARLLCETLLEPGCQLESLWVKSCSFTAACCPHFSSVLAQNRFLLELQ 342

Qy        980 LTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQ 1039
              :::| | | ||  ||:|| |  |||  | |  | ::  | :|:  | |  |  |:|
Db        343 ISNNRLEDAGVRELCQGLGQPGSVLRVLWLADCDVSDSSCSSLAATLLANHSLRELDLSN 402

Qy       1040 NNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKP--RVV 1090
              |    |:::|  :   |   |: : |:   :  ::   |: ::  ||  ||:
Db        403 NCLGDAGILQLVESVRQPGCLLEQLVLYDIYWSEEMEDRLQALEKDKPSLRVI 455


RESULT 11
US-08-910-731-6
; Sequence 6, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  461 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  peptide
US-08-910-731-6

  Query Match             8.6%;  Score 607.5;  DB 2;  Length 461;
  Best Local Similarity   33.1%;  Pred. No. 1.6e-50;
  Matches  144;  Conservative   80;  Mismatches  206;  Indels    5;  Gaps    3;

Qy        659 EACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTC 718
              : | || |   |  | | : :|  | |  :| | :|:| |: | :  :  :   |: |:|
Db         28 QQCQVVRL--DDCGLTEARCKDISSALRVNPALAELNLRSNELGDVGVHCVLQGLQTPSC 85

Qy        719 KIQTLMFRNAQIT-PGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLE 777
              |||  |  :|  :|  |   |   :     |: |:|    | :  ::: || |  |:| ||
Db         86 KIQKLSLQNCCLTGAGCGVLSSTLRTLPTLQELHLSDNLLGDAGLQLLCEGLLDPQCRLE 145

Qy        778 SLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLI 837
              |:|: | |: |    :: :|   |  | |::: | : : || |   |: | | |: |
Db        146 KLQLEYCSLSAASCEPLASVLRAKPDFKELTVSNNDINEAGVRVLCQGLKDSPCQLEALK 205

Qy        838 LEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQ 897
              || ||:|:  |: |   : |  ||  | | :| ||: |:  ||  :  |   |: | : :
Db        206 LESCGVTSDNCRDLCGIVASKASLRELALGSNKLGDVGMAELCPGLLHPSSRLRTLWIWE 265

Qy        898 CHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHL 957
              | :   ||| |   |      |  |||: | : | | :|||| : || | |: | :  |
Db        266 CGITAKGCGDLCRVLRAKESLKELSLAGNELGDEGARLLCETLLEPGCQLESLWVKSCSF 325

Qy        958 TAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSD 1017
              |||||   | |:::: | |  | :::| | | ||  ||:|| |  |||  | |  | ::
Db        326 TAACCPHFSSVLAQNRFLLELQISNNRLEDAGVRELCQGLGQPGSVLRVLWLADCDVSDS 385

Qy       1018 CCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRK 1077
              | :|:  |  |  |  |:|  |      |:::|  :   |   |: : |:  :  ::
Db        386 SCSSLAATLLANHSLRELDLSNNCLGDAGILQLVESVRQPGCLLEQLVLYDIYWSEEMED 445

Qy       1078 LLEEVQLLKP--RVV 1090
              |: ::  ||  ||:
Db        446 RLQALEKDKPSLRVI 460


RESULT 12
US-09-245-281-43
; Sequence 43, Application US/09245281
; Patent No. 6369196
; GENERAL INFORMATION:
;  APPLICANT: Bertin, John
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 07334/118001
;  CURRENT APPLICATION NUMBER: US/09/245,281
;  CURRENT FILING DATE: 1999-02-05
;  EARLIER APPLICATION NUMBER: US 09/207,359
;  EARLIER FILING DATE: 1998-12-08
;  EARLIER APPLICATION NUMBER: US 09/099,041
;  EARLIER FILING DATE: 1998-06-17
;  EARLIER APPLICATION NUMBER: US 09/019,942
;  EARLIER FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
;   LENGTH: 953
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-245-281-43

  Query Match             5.3%;  Score 374.5;  DB 3;  Length 953;
  Best Local Similarity   22.7%;  Pred. No. 6.2e-27;
  Matches  232;  Conservative  150;  Mismatches  398;  Indels  241;  Gaps   44;

Qy         54 NVECLA--LLLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQAMEQEGATAAE 111
              | :||   || : |: |           |:  :         | ::||   :: :|   :|
Db         36 NTQCLVDNLLENGYFSA----------EDAEIVCACPTKPDKVRKILDLVQSKGEEVSE 84

Qy        112 ---TEEQEISQA-------MEQEGATAAE---------------TEEQGH--GGDTWDY 143
                  |::  |       : : | : ::                 |::  |  | |
Db         85 FFLYVLQQLEDAYVDLRLWLSEIGFSPSQLIRTKTIVNTDPVSRYTQQLRHQLGRD---- 140

Qy        144 KSHVMTKFAEEEDVRRSFENTAADWPEMQTLAG--AFDSDRWGF--------------- 185
                | |  :|::||:   | |      | || |   |:::  |
Db        141 -SKFMLCYAQKEDL--LLEET-----YMDTLMGLVGFNNENLGSLGGLDCLLDHSTGVLN 192

Qy        186 -RPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKES---SVT 241
                 || : | :|:||| | :|:   || | |       : |    |     |||   |:
Db        193 EHGETVFVFGDAGVGKSMLLQRLQSLWASGRL-TSTAKFFFHFRCRMFSCFKESDMLSLQ 251
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Qy        242 EFISREW----PDSQAPVTEIMSRPERLLFIIDGFDDLGS--VLNNDTKLCKDWAEKQPP 295
Db        252 DLLFKHFCYPEQDPEEVFSFLLRFPHTALPTFDGLDELHSDFDLSRVPDSCCPW-EPAHP 310

Qy        296 FTLIRSLLRKVLLPESFLIVTVR---DVGTEKLKSEVVSPRYLLVRGISGEQRIHL---- 348
Db        311 LVLLANLLSGRLLKGAGKLLTARTGVEVPRQLLRKKV------LLRGFSPS---HLRAYA 361

Qy        349 ---LLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQ-LQDVVGESVAPFNQ 404
Db        362 RRMFPERTAQEHL----LQQLDANPNLCSLCGVPLFCWIIFRCFQHFQTVFEGSSSQLPD 417

Qy        405 TLTGLHAAFV------FHQLTPRGVVRRCLNLEERVV------LKRFCRMAVEGVWNRKS 452
Db        418 CAVTLTDVFLLVTEVHLNRPQPSSLVQRNTRSPAETLRAGWRTLHALGEVAHRGTDKSLF 477

Qy        453 VFDGDDLMVQGLGESELRALFHMNILLPDSHCE--EYYTFFHLSLQDFCAALYYVLEGLE 510
Db        478 VFGQEEVQASKLQEGDLQLGFLR--ALPDVGPEQGQSYEFFHLTLQAFFTAFFLVADDKV 535

Qy        511 IEPALCPLYVEKTKRSMELKQAGFHI----------------------HSLWMKRFLFG 547
Db        536 STRELLRFFREWTSPG-EATSSSCHSSFFSFQCLGGRSRLGPDPFRNKDHFQFTNLFVCG 594

Qy        548 LVSEDVRRPLEVLLGCPVPLGV---KQKLLHWV-------SLLGQQPNATTPG------- 590
Db        595 LLAKARQKLLRQL----VPKAILRRKRKAL-WAHLFASLRSYLKSLPRVQSGGFNQVHAM 649

Qy        591 -DTLDAFHCLFETQDKEFVRLALNSFQEVWLPI----NQNLDLIASSFCLQHCPYLRKIR 645
Db        650 PTFLWMLRCIYETQSQKVGRLAARGISADYLKLAFCNACSADCSALSFVLHH--FHRQLA 707

Qy        646 VDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERA 705
Db        708 LDLDNNNLNDYGVQ--ELQPCFSR--------------------LTVIRLSVNQITDTG 744

Qy        706 MKTLCAKLRHPTCKIQTLM-FRNAQITP-GVQHLWRIVMANRNLRSLNLGGTHLKEEDVR 763
Db        745 VKVLCEEL--TKYKIVTFLGLYNNQITDIGARYVAQILDECRGLKHLKLGKNRITSEGGK 802

Qy        764 MACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLS 823
Db        803 CVALAVKN----------------------------STSIVDVGMWGNQIGDEGAKAFA 833

Qy        824 DALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSM 883
Db        834 EALK-DHPSLTTLSLAFNGISPEGGKSLAQALKQNTTLTVIWLTKNELNDESAECFAEML 892

Qy        884 RLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVE-------DNGVKLL 936
Db        893 RV-NQTLRHLWLIQNRITAKGTAQLARALQKNTAITEICLNGNLIKPEEAKVFENEKRII 951

Qy        937 C 937
Db        952 C 952
```

```
RESULT 13
US-09-207-359B-43
; Sequence 43, Application US/09207359B
; Patent No. 6469140
; GENERAL INFORMATION:
;  APPLICANT: Bertin, John
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
;  TITLE OF INVENTION:  PROTEIN FAMILY AND USES THEREOF
;  FILE REFERENCE: 07334-112001
;  CURRENT APPLICATION NUMBER: US/09/207,359B
;  CURRENT FILING DATE:  1998-12-08
;  PRIOR APPLICATION NUMBER: US 09/099,041
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: US 09/019,942
;  PRIOR FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
;   LENGTH: 953
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-207-359B-43

  Query Match             5.3%;  Score 374.5;  DB 4;  Length 953;
  Best Local Similarity   22.7%;  Pred. No. 6.2e-27;
  Matches  232;  Conservative  150;  Mismatches  398;  Indels  241;  Gaps   44;

Qy         54 NVECLA--LLLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQAMEQEGATAAE 111
Db         36 NTQCLVDNLLENGYFSA----------EDAEIVCACPTKPDKVRKILDLVQSKGEEVSE 84

Qy        112 ---TEEQEISQA-------MEQEGATAAE---------------TEEQGH--GGDTWDY 143
Db         85 FFLYVLQQLEDAYVDLRLWLSEIGFSPSQLIRTKTIVNTDPVSRYTQQLRHQLGRD---- 140

Qy        144 KSHVMTKFAEEEDVRRSFENTAADWPEMQTLAG--AFDSDRWGF---------------- 185
Db        141 -SKFMLCYAQKEDL--LLEET-----YMDTLMGLVGFNNENLGSLGGLDCLLDHSTGVLN 192

Qy        186 -RPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKES---SVT 241
Db        193 EHGETVFVFGDAGVGKSMLLQRLQSLWASGRL-TSTAKFFFHFRCRMFSCFKESDMLSLQ 251

Qy        242 EFISREW----PDSQAPVTEIMSRPERLLFIIDGFDDLGS--VLNNDTKLCKDWAEKQPP 295
Db        252 DLLFKHFCYPEQDPEEVFSFLLRFPHTALFTFDGLDELHSDFDLSRVPDSCCPW-EPAHP 310

Qy        296 FTLIRSLLRKVLLPESFLIVTVR---DVGTEKLKSEVVSPRYLLVRGISGEQRIHL---- 348
Db        311 LVLLANLLSGRLLKGAGKLLTARTGVEVPRQLLRKKV------LLRGFSPS---HLRAYA 361

Qy        349 ---LLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQ-LQDVVGESVAPFNQ 404
Db        362 RRMFPERTAQEHL----LQQLDANPNLCSLCGVPLFCWIIFRCFQHFQTVFEGSSSQLPD 417

Qy        405 TLTGLHAAFV------FHQLTPRGVVRRCLNLEERVV------LKRFCRMAVEGVWNRKS 452
Db        418 CAVTLTDVFLLVTEVHLNRPQPSSLVQRNTRSPAETLRAGWRTLHALGEVAHRGTDKSLF 477

Qy        453 VFDGDDLMVQGLGESELRALFHMNILLPDSHCE--EYYTFFHLSLQDFCAALYYVLEGLE 510
Db        478 VFGQEEVQASKLQEGDLQLGFLR--ALPDVGPEQGQSYEFFHLTLQAFFTAFFLVADDKV 535

Qy        511 IEPALCPLYVEKTKRSMELKQAGFHI----------------------HSLWMKRFLFG 547
Db        536 STRELLRFFREWTSPG-EATSSSCHSSFFSFQCLGGRSRLGPDPFRNKDHFQFTNLFVCG 594

Qy        548 LVSEDVRRPLEVLLGCPVPLGV---KQKLLHWV-------SLLGQQPNATTPG------- 590
Db        595 LLAKARQKLLRQL----VPKAILRRKRKAL-WAHLFASLRSYLKSLPRVQSGGFNQVHAM 649

Qy        591 -DTLDAFHCLFETQDKEFVRLALNSFQEVWLPI----NQNLDLIASSFCLQHCPYLRKIR 645
Db        650 PTFLWMLRCIYETQSQKVGRLAARGISADYLKLAFCNACSADCSALSFVLHH--FHRQLA 707

Qy        646 VDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERA 705
Db        708 LDLDNNNLNDYGVQ--ELQPCFSR--------------------LTVIRLSVNQITDTG 744

Qy        706 MKTLCAKLRHPTCKIQTLM-FRNAQITP-GVQHLWRIVMANRNLRSLNLGGTHLKEEDVR 763
Db        745 VKVLCEEL--TKYKIVTFLGLYNNQITDIGARYVAQILDECRGLKHLKLGKNRITSEGGK 802

Qy        764 MACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLS 823
Db        803 CVALAVKN----------------------------STSIVDVGMWGNQIGDEGAKAFA 833

Qy        824 DALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSM 883
```

```
Db        834 EALK-DHPSLTTLSLAFNGISPEGGKSLAQALKQNTTLTVIWLTKNELNDESAECFAEML 892

Qy        884 RLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVE-------DNGVKLL 936
              |: : :|: | | |  :   |  || ||  |: :| : |: | ::       :|  :::
Db        893 RV-NQTLRHLWLIQNRITAKGTAQLARALQKNTAITEICLNGNLIKPEEAKVFENEKRII 951

Qy        937 C 937
              |
Db        952 C 952


RESULT 14
US-09-340-620A-43
; Sequence 43, Application US/09340620A
; Patent No. 6482933
; GENERAL INFORMATION:
;  APPLICANT: Bertin, John
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
;  FILE REFERENCE: 07334-124001
;  CURRENT APPLICATION NUMBER: US/09/340,620A
;  CURRENT FILING DATE:  1999-06-28
;  PRIOR APPLICATION NUMBER: US 09/245,281
;  PRIOR FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: US 09/207,359
;  PRIOR FILING DATE: 1998-12-08
;  PRIOR APPLICATION NUMBER: US 09/099,041
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: US 09/019,942
;  PRIOR FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 71
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
;   LENGTH: 953
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-340-620A-43

  Query Match             5.3%;  Score 374.5;  DB 4;  Length 953;
  Best Local Similarity   22.7%;  Pred. No. 6.2e-27;
  Matches  232;  Conservative  150;  Mismatches  398;  Indels  241;  Gaps   44;

Qy         54 NVECLA--LLLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQAMEQEGATAAE 111
              | :||   || : |: |           |:  :        | ::||   :: :|   :|
Db         36 NTQCLVDNLLENGYFSA----------EDAEIVCACPTKPDKVRKILDLVQSKGEEVSE 84

Qy        112 ---TEEQEISQA-------MEQEGATAAE---------------TEEQGH--GGDTWDY 143
                 |::  |       : : | : ::                |::  |  | |
Db         85 FFLYVLQQLEDAYVDLRLWLSEIGFSPSQLIRTKTIVNTDPVSRYTQQLRHQLGRD---- 140

Qy        144 KSHVMTKFAEEEDVRRSFENTAADWPEMQTLAG--AFDSDRWGF---------------- 185
                |  |  :|::||:    | |       | || |   |:::  |
Db        141 -SKFMLCYAQKEDL--LLEET-----YMDTLMGLVGFNNENLGSLGGLDCLLDHSTGVLN 192

Qy        186 -RPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKES---SVT 241
                || : | :|:||| | :|:   || | |     : |    |     |||   |:
Db        193 EHGETVFVFGDAGVGKSMLLQRLQSLWASGRL-TSTAKFFFHFRCRMFSCFKESDMLSLQ 251

Qy        242 EFISREW----PDSQAPVTEIMSRPERLLFIIDGFDDLGS--VLNNDTKLCKDWAEKQPP 295
              : : : :      | :   : ::  |   ||  || |:| |   |:      |  | |   |
Db        252 DLLFKHFCYPEQDPEEVFSFLLRFPHTALFTFDGLDELHSDFDLSRVPDSCCPW-EPAHP 310

Qy        296 FTLIRSLLRKVLLPESFLIVTVR---DVGTEKLKSEVVSPRYLLVRGISGEQRIHL---- 348
                |: :||   ||  :  ::| |   :|  : |: :|       |:|| |     ||
Db        311 LVLLANLLSGRLLKGAGKLLTARTGVEVPRQLLRKKV------LLRGFSPS---HLRAYA 361

Qy        349 ---LLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQ-LQDVVGESVAPFNQ 404
                 ||   ||      |: :  |  |   | ||    :|     |  | |   | :
Db        362 RRMFPERTAQEHL----LQQLDANPNLCSLCGVPLFCWIIFRCFQHFQTVFEGSSSQLPD 417

Qy        405 TLTGLHAAFV------FHQLTPRGVVRRCLNLEERVV------LKRFCRMAVEGVWNRKS 452
                  |   |:       ::  |  :|:|        :       |     :|  |
Db        418 CAVTLTDVFLLVTEVHLNRPQPSSLVQRNTRSPAETLRAGWRTLHALGEVAHRGTDKSLF 477

Qy        453 VFDGDDLMVQGLGESELRALFHMNILLPDSHCE--EYYTFFHLSLQDFCAALYYVLEGLE 510
              ||  :::    | | :|:  |     |||   |  : | ||||:|| |  | : | :
Db        478 VFGQEEVQASKLQEGDLQLGFLR--ALPDVGPEQGQSYEFFHLTLQAFFTAFFLVADDKV 535

Qy        511 IEPALCPLYVEKTKRSMELKQAGFHI----------------------HSLWMKRFLFG 547
                  |   : | |    |   : |                        |  :   |: |
Db        536 STRELLRFFREWTSPG-EATSSSCHSSFFSFQCLGGRSRLGPDPFRNKDHFQFTNLFVCG 594

Qy        548 LVSEDVRRPLEVLLGCPVPLGV---KQKLLHWV-------SLLGQQPNATTPG------- 590
              |:::  :: | |    ||  :   |:| | |       | |   |  : |
Db        595 LLAKARQKLLRQL----VPKAILRRKRKAL-WAHLFASLRSYLKSLPRVQSGGFNQVHAM 649

Qy        591 -DTLDAFHCLFETQDKEFVRLALNSFQEVWLPI----NQNLDLIASSFCLQHCPYLRKIR 645
               |    |:|||| ::  |||       :| :      : |  | || | |  : |::
Db        650 PTFLWMLRCIYETQSQKVGRLAARGISADYLKLAFCNACSADCSALSFVLHH--FHRQLA 707

Qy        646 VDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERA 705
              :|:      |   :   : | : |                       |  : |  : :|:
Db        708 LDLDNNNLNDYGVQ--ELQPCFSR--------------------LTVIRLSVNQITDTG 744

Qy        706 MKTLCAKLRHPTCKIQTLM-FRNAQITP-GVQHLWRIVMANRNLRSLNLGGTHLKEEDVR 763
              :| || :|     || | :   | |||  | ::: :|:    | |: | ||   :  | :
Db        745 VKVLCEEL--TKYKIVTFLGLYNNQITDIGARYVAQILDECRGLKHLKLGKNRITSEGGK 802

Qy        764 MACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLS 823
                |:|:                                  | |:  : : ||:: |:|    :
Db        803 CVALAVKN----------------------------STSIVDVGMWGNQIGDEGAKAFA 833

Qy        824 DALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSM 883
              :||:    :|  | |   ||:  | :||| ||  | :|| : |: | | :|       :
Db        834 EALK-DHPSLTTLSLAFNGISPEGGKSLAQALKQNTTLTVIWLTKNELNDESAECFAEML 892

Qy        884 RLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVE-------DNGVKLL 936
              |: : :|: | | |  :   |  || ||  |: :| : |: | ::       :|  :::
Db        893 RV-NQTLRHLWLIQNRITAKGTAQLARALQKNTAITEICLNGNLIKPEEAKVFENEKRII 951

Qy        937 C 937
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Db        952 C 952


RESULT 15
US-09-865-364-43
; Sequence 43, Application US/09865364
; Patent No. 6613521
; GENERAL INFORMATION:
;  APPLICANT: Bertin, John
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
;  TITLE OF INVENTION:  PROTEIN FAMILY AND USES THEREOF
;  FILE REFERENCE: 07334-112001
;  CURRENT APPLICATION NUMBER: US/09/865,364
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 09/207,359
;  PRIOR FILING DATE: 1998-12-08
;  PRIOR APPLICATION NUMBER: US 09/099,041
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: US 09/019,942
;  PRIOR FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
;   LENGTH: 953
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-865-364-43

  Query Match             5.3%;  Score 374.5;  DB 4;  Length 953;
  Best Local Similarity   22.7%;  Pred. No. 6.2e-27;
  Matches  232;  Conservative  150;  Mismatches  398;  Indels  241;  Gaps   44;

Qy         54 NVECLA--LLLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQAMEQEGATAAE 111
              | :||   || : |: |           |:  :        | ::||   :: :|   :|
Db         36 NTQCLVDNLLENGYFSA----------EDAEIVCACPTKPDKVRKILDLVQSKGEEVSE 84
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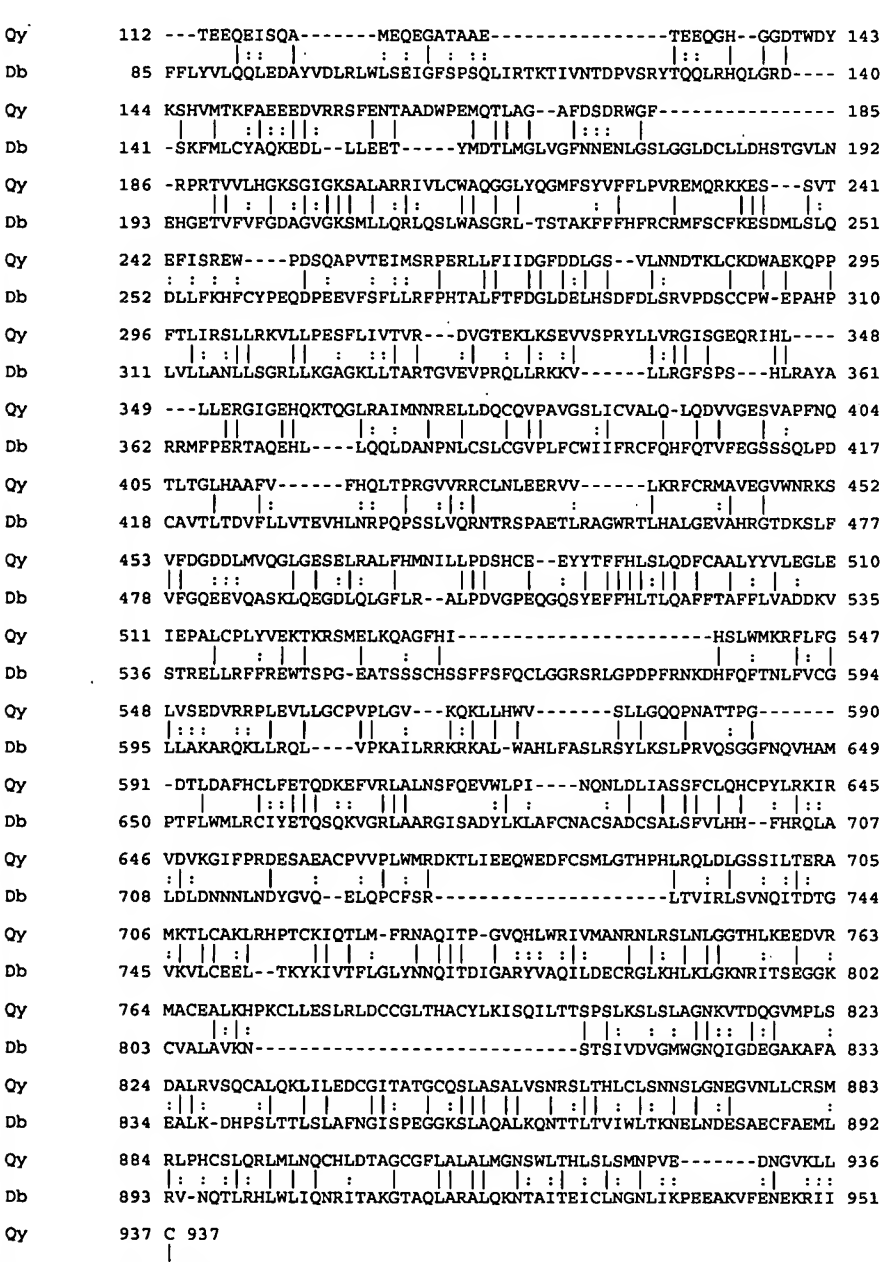

Search completed: July 19, 2005, 12:03:54
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 19, 2005, 11:19:57 ; Search time 475 Seconds
(without alignments)
1098.368 Million cell updates/sec

Title: US-10-066-521-6
Perfect score: 7074
Sequence: 1 MEGDKSLTFSSYGLQWCLYE.....DDHSGVSWSLGAAGLEGLVS 1344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1736639 seqs, 388188149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7074	100.0	1344	14	US-10-124-498-6	Sequence 6, Appli
2	7074	100.0	1344	14	US-10-066-521-6	Sequence 6, Appli
3	5756	81.4	1162	14	US-10-216-645-2	Sequence 2, Appli
4	5756	81.4	1162	15	US-10-416-642-1	Sequence 1, Appli
5	5741.5	81.2	1200	15	US-10-399-443-24	Sequence 24, Appl
6	5741.5	81.2	1200	15	US-10-677-943-24	Sequence 24, Appl
7	5741.5	81.2	1200	16	US-10-860-761-4	Sequence 4, Appli
8	5683.5	80.3	1143	14	US-10-216-645-4	Sequence 4, Appli
9	5113.5	72.3	1033	15	US-10-092-900A-348	Sequence 348, App
10	3318.5	46.9	682	15	US-10-407-866-96	Sequence 96, Appl
11	2688	38.0	1111	14	US-10-216-645-5	Sequence 5, Appli
12	2577	36.4	1111	15	US-10-399-443-6	Sequence 6, Appli
13	2577	36.4	1111	15	US-10-677-943-6	Sequence 6, Appli
14	1940	27.4	385	15	US-10-399-443-2	Sequence 2, Appli
15	1940	27.4	385	15	US-10-677-943-2	Sequence 2, Appli
16	1885.5	26.7	1093	16	US-10-794-342-13	Sequence 13, Appl
17	1434	20.3	994	10	US-09-965-621-16	Sequence 16, Appl
18	1434	20.3	994	14	US-10-124-498-24	Sequence 24, Appl
19	1434	20.3	994	14	US-10-066-521-24	Sequence 24, Appl
20	1434	20.3	994	15	US-10-407-866-16	Sequence 16, Appl
21	1434	20.3	994	16	US-10-781-294-16	Sequence 16, Appl
22	1402	19.8	924	15	US-10-357-820-52	Sequence 52, Appl
23	1332.5	18.8	991	16	US-10-794-342-14	Sequence 14, Appl
24	1320.5	18.7	1035	10	US-09-965-621-24	Sequence 24, Appl
25	1320.5	18.7	1035	15	US-10-407-866-24	Sequence 24, Appl
26	1320.5	18.7	1035	16	US-10-781-294-24	Sequence 24, Appl
27	1315.5	18.6	919	15	US-10-094-749-2718	Sequence 2718, Ap
28	1314.5	18.6	919	15	US-10-161-493-4	Sequence 4, Appli
29	1314.5	18.6	919	16	US-10-398-037-7	Sequence 7, Appli
30	1313.5	18.6	1036	16	US-10-794-342-18	Sequence 18, Appl
31	1303.5	18.4	1061	14	US-10-124-498-18	Sequence 18, Appl
32	1303.5	18.4	1061	14	US-10-066-521-18	Sequence 18, Appl
33	1301.5	18.4	1027	15	US-10-407-866-68	Sequence 68, Appl
34	1289.5	18.2	858	9	US-09-848-035-8	Sequence 8, Appli
35	1289.5	18.2	858	9	US-09-986-224-8	Sequence 8, Appli
36	1283	18.1	258	15	US-10-399-443-4	Sequence 4, Appli
37	1283	18.1	258	15	US-10-677-943-4	Sequence 4, Appli
38	1255	17.7	1032	16	US-10-882-761-33	Sequence 33, Appl
39	1255	17.7	1034	13	US-10-127-516-5	Sequence 5, Appli
40	1255	17.7	1034	13	US-10-027-629-5	Sequence 5, Appli
41	1255	17.7	1034	14	US-10-028-374-18	Sequence 18, Appl
42	1255	17.7	1034	14	US-10-132-967-5	Sequence 5, Appli
43	1255	17.7	1034	14	US-10-183-770-18	Sequence 18, Appl
44	1255	17.7	1034	15	US-10-264-958B-22	Sequence 22, Appl
45	1248.5	17.6	1062	14	US-10-239-663-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-10-124-498-6
; Sequence 6, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-124-498-6

Query Match 100.0%; Score 7074; DB 14; Length 1344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60

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Qy          61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQAMEQEGATAAETEEQEISQA 120
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Db          61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQAMEQEGATAAETEEQEISQA 120

Qy         121 MEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDS 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 MEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDS 180

Qy         181 DRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSV 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 DRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSV 240

Qy         241 TEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIR 300
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Db         241 TEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIR 300

Qy         301 SLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 SLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKT 360

Qy         361 QGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTP 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 QGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTP 420

Qy         421 RGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLP 480
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Qy         661 CPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKI 720
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Db         661 CPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKI 720

Qy         721 QTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLR 780
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Db         841 CGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHL 900

Qy         901 DTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAA 960
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Db         901 DTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAA 960

Qy         961 CCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCE 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        1021 ALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLE 1080
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RESULT 2
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; Sequence 6, Application US/10066521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-334001
; CURRENT APPLICATION NUMBER: US/10/066,521
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-521-6

Query Match 100.0%; Score 7074; DB 14; Length 1344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy           1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60
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Db           1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60

Qy          61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQAMEQEGATAAETEEQEISQA 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQAMEQEGATAAETEEQEISQA 120

Qy         121 MEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDS 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         181 DRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSV 240
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Qy         241 TEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIR 300
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Db         241 TEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIR 300

Qy         301 SLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 SLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKT 360

Qy         361 QGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTP 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 QGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTP 420
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Qy        421 RGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 RGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLP 480

Qy        481 DSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLW 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 DSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLW 540

Qy        541 MKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLF 600

Qy        601 ETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEA 660

Qy        661 CPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKI 720

Qy        721 QTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 QTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLR 780

Qy        781 LDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILED 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILED 840

Qy        841 CGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHL 900

Qy        901 DTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 DTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAA 960

Qy        961 CCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCE 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCE 1020

Qy       1021 ALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLE 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLE 1080

Qy       1081 EVQLLKPRVVIDGSWHSFDEDDRHKIGLTFRLPESRAWPCALLWGMNPEQKKRVSLLAGD 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 EVQLLKPRVVIDGSWHSFDEDDRHKIGLTFRLPESRAWPCALLWGMNPEQKKRVSLLAGD 1140

Qy       1141 FKSSTRFAKSLCLATANGESQRVDNVEQSSPQPMAGTEHKQDKMLSVGYSGAWSETAELE 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 FKSSTRFAKSLCLATANGESQRVDNVEQSSPQPMAGTEHKQDKMLSVGYSGAWSETAELE 1200

Qy       1201 GLGSNSADHDHGGMAWSLGRELSSRGLCPTVLMTTAVCPGHWERLGSRGWCLNSADDHSG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GLGSNSADHDHGGMAWSLGRELSSRGLCPTVLMTTAVCPGHWERLGSRGWCLNSADDHSG 1260

Qy       1261 VSWSLGAAGLEGLVSNSADDHSGVAWSLGAAGLEGLVSNSADDHSGVSWSLGAAGLEGLV 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 VSWSLGAAGLEGLVSNSADDHSGVAWSLGAAGLEGLVSNSADDHSGVSWSLGAAGLEGLV 1320

Qy       1321 SNSADDHSGVSWSLGAAGLEGLVS 1344
              ||||||||||||||||||||||||
Db       1321 SNSADDHSGVSWSLGAAGLEGLVS 1344
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RESULT 3
US-10-216-645-2
; Sequence 2, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LESSL, MONIKA
; APPLICANT: PETERS-KOTTIG, MICHAELE
; APPLICANT: BECKMANN, GEORG
; TITLE OF INVENTION: HUMAN MATER PROTEINS
; FILE REFERENCE: SCH-1910
; CURRENT APPLICATION NUMBER: US/10/216,645
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-645-2

Query Match 81.4%; Score 5756; DB 14; Length 1162;
Best Local Similarity 95.2%; Pred. No. 0;
Matches 1102; Conservative 2; Mismatches 0; Indels 54; Gaps 1;

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Qy          1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60

Qy         61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMK---------------------- 96
              ||||||||||||||||||||||||||||||||||||
Db         61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKNSPEDPEATMTDQGPSKEKVPENK 120

Qy         97 ------------------------------KISQAMEQEGATAAETEEQEISQAMEQEGA 126
                                           :||||||||||||||||||||||||||||||
Db        121 YGMTKLILGVSDISDSNNKHKYVGIHSSFAEISQAMEQEGATAAETEEQEISQAMEQEGA 180

Qy        127 TAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFR 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFR 240

Qy        187 PRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISR 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 PRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISR 300

Qy        247 EWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKV 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 EWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKV 360

Qy        307 LLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAI 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 LLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAI 420

Qy        367 MNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRR 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 MNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRR 480

Qy        427 CLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEE 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEE 540

Qy        487 YYTFFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLF 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 YYTFFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLF 600

Qy        547 GLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKE 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKE 660

Qy        607 FVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPL 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 FVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPL 720

Qy        667 WMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFR 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 WMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFR 780

Qy        727 NAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGL 786
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 NAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGL 840

Qy        787 THACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITAT 846
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 THACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITAT 900

Qy        847 GCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCG 906
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCG 960

Qy        907 FLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLS 966
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 FLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLS 1020

Qy        967 CVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLAL 1026
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLAL 1080

Qy       1027 SCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLK 1086
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 SCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLK 1140

Qy       1087 PRVVIDGSWHSFDEDDRH 1104
                |||||||||||||||||:
Db       1141 PRVVIDGSWHSFDEDDRY 1158


RESULT 4
US-10-416-642-1
; Sequence 1, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  ARVIZU, Chandra
;  TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
;  FILE REFERENCE: PF-0842 PCT
;  CURRENT APPLICATION NUMBER: US/10/416,642
;  CURRENT FILING DATE:  2003-05-13
;  PRIOR APPLICATION NUMBER: 60/249,407
;  PRIOR FILING DATE: 2000-11-15
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 1162
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CD1
US-10-416-642-1

  Query Match             81.4%;  Score 5756;  DB 15;  Length 1162;
  Best Local Similarity   95.2%;  Pred. No. 0;
  Matches 1102;  Conservative    2;  Mismatches    0;  Indels   54;  Gaps    1;

Qy           1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60

Qy          61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMK---------------------- 96
                |||||||||||||||||||||||||||||||||||
Db          61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKNSPEDPEATMTDQGPSKEKVPENK 120

Qy          97 -----------------------------KISQAMEQEGATAAETEEQEISQAMEQEGA 126
                                            :||||||||||||||||||||||||||||||
Db         121 YGMTKLILGVSDISDSNNKHKYVGIHSSFAEISQAMEQEGATAAETEEQEISQAMEQEGA 180

Qy         127 TAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFR 186
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 TAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFR 240

Qy         187 PRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISR 246
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 PRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISR 300

Qy         247 EWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKV 306
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 EWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKV 360

Qy         307 LLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAI 366
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 LLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAI 420

Qy         367 MNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRR 426
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 MNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRR 480

Qy         427 CLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEE 486
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEE 540

Qy         487 YYTFFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLF 546
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 YYTFFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLF 600

Qy         547 GLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKE 606
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKE 660

Qy         607 FVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPL 666
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 FVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPL 720

Qy         667 WMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFR 726
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 WMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFR 780

Qy         727 NAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGL 786
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 NAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGL 840

Qy         787 THACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITAT 846
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 THACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITAT 900

Qy         847 GCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCG 906
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCG 960

Qy         907 FLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLS 966
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 FLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLS 1020

Qy         967 CVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLAL 1026
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 CVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLAL 1080

Qy        1027 SCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLK 1086
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 SCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLK 1140

Qy        1087 PRVVIDGSWHSFDEDDRH 1104
                |||||||||||||||||:
Db        1141 PRVVIDGSWHSFDEDDRY 1158


RESULT 5
US-10-399-443-24
; Sequence 24, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute o
;  APPLICANT:  Health
```

```
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
;   LENGTH: 1200
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-399-443-24

  Query Match             81.2%;  Score 5741.5;  DB 15;  Length 1200;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 1098;  Conservative    3;  Mismatches    3;  Indels   41;  Gaps    1;

Qy          1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 111

Qy         61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKK---------------------- 97
              |||||||||||||||||||||||||||||||||||:
Db        112 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKRHSPEDPEATMTDQGPSKEKVPGI 171

Qy         98 ------------------ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGD 139
                                 |||||||||||||||||||||||||||||||||||||||||||
Db        172 SQAVQQDSATAAETKEQEISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGD 231

Qy        140 TWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIG 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 TWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIG 291

Qy        200 KSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIM 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 KSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIM 351

Qy        260 SRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRD 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 SRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRD 411

Qy        320 VGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVP 379
              |||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db        412 VGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIINNRELLDQCQVP 471

Qy        380 AVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRF 439
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        472 AVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFAFHQLTPRGVVRRCLNLEERVVLKRF 531

Qy        440 CRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFC 591

Qy        500 AALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEV 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 AALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEV 651

Qy        560 LLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVW 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 LLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVW 711

Qy        620 LPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWE 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 LPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWE 771

Qy        680 DFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWR 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 DFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWR 831

Qy        740 IVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        832 IVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILT 891

Qy        800 TSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNR 859
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        892 TSPSLKSLSLAGNKVTDQGVTPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNR 951

Qy        860 SLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLT 919
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        952 SLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGSLALALMGNSWLT 1011

Qy        920 HLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLD 979
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 HLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLD 1071

Qy        980 LTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQ 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 LTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQ 1131

Qy       1040 NNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFD 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 NNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFD 1191

Qy       1100 EDDRH 1104
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Db       1192 EDDRY 1196


RESULT 6
US-10-677-943-24
; Sequence 24, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
;   LENGTH: 1200
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-677-943-24

  Query Match             81.2%;  Score 5741.5;  DB 15;  Length 1200;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 1098;  Conservative    3;  Mismatches    3;  Indels   41;  Gaps    1;

Qy          1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 111

Qy         61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKK---------------------- 97
              |||||||||||||||||||||||||||||||||||:
Db        112 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKRHSPEDPEATMTDQGPSKEKVPGI 171

Qy         98 ------------------ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGD 139
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                                 ||||||||||||||||||||||||||||||||||||||||||||
Db        172 SQAVQQDSATAAETKEQEISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGD 231

Qy        140 TWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIG 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 TWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIG 291

Qy        200 KSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIM 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 KSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIM 351

Qy        260 SRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRD 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 SRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRD 411

Qy        320 VGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVP 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db        412 VGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIINNRELLDQCQVP 471

Qy        380 AVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRF 439
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        472 AVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFAFHQLTPRGVVRRCLNLEERVVLKRF 531

Qy        440 CRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFC 591

Qy        500 AALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEV 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 AALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEV 651

Qy        560 LLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVW 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 LLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVW 711

Qy        620 LPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWE 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 LPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWE 771

Qy        680 DFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWR 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 DFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWR 831

Qy        740 IVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        832 IVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILT 891

Qy        800 TSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNR 859
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        892 TSPSLKSLSLAGNKVTDQGVTPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNR 951

Qy        860 SLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLT 919
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        952 SLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGSLALALMGNSWLT 1011

Qy        920 HLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLD 979
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 HLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLD 1071

Qy        980 LTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQ 1039
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1072 LTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQ 1131

Qy       1040 NNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFD 1099
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 NNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFD 1191

Qy       1100 EDDRH 1104
              ||||:
Db       1192 EDDRY 1196


RESULT 7
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US-10-860-761-4
; Sequence 4, Application US/10860761
; Publication No. US20040248775A1
; GENERAL INFORMATION:
;  APPLICANT: WYETH
;  TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS
;  FILE REFERENCE: AM101318
;  CURRENT APPLICATION NUMBER: US/10/860,761
;  CURRENT FILING DATE:  2004-06-03
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 1200
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-860-761-4

  Query Match             81.2%;  Score 5741.5;  DB 16;  Length 1200;
  Best Local Similarity   95.9%;  Pred. No. 0;
  Matches 1098;  Conservative    3;  Mismatches    3;  Indels   41;  Gaps    1;

Qy          1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 111

Qy         61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKK---------------------- 97
              |||||||||||||||||||||||||||||||||||:
Db        112 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKRHSPEDPEATMTDQGPSKEKVPGI 171

Qy         98 ------------------ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGD 139
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Db        172 SQAVQQDSATAAETKEQEISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGD 231

Qy        140 TWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIG 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 TWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIG 291

Qy        200 KSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIM 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 KSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIM 351

Qy        260 SRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRD 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 SRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRD 411

Qy        320 VGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVP 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
Db        412 VGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIINNRELLDQCQVP 471

Qy        380 AVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRF 439
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        472 AVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFAFHQLTPRGVVRRCLNLEERVVLKRF 531

Qy        440 CRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFC 591

Qy        500 AALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEV 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 AALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEV 651

Qy        560 LLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVW 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 LLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVW 711

Qy        620 LPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWE 679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 LPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWE 771

Qy        680 DFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWR 739
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 DFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWR 831
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Qy        740 IVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILT 799
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        832 IVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILT 891

Qy        800 TSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNR 859
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        892 TSPSLKSLSLAGNKVTDQGVTPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNR 951

Qy        860 SLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLT 919
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        952 SLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGSLALALMGNSWLT 1011

Qy        920 HLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLD 979
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1012 HLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLD 1071

Qy        980 LTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQ 1039
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Db       1072 LTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQ 1131

Qy       1040 NNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFD 1099
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1132 NNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFD 1191

Qy       1100 EDDRH 1104
              ||||:
Db       1192 EDDRY 1196
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RESULT 8
US-10-216-645-4
; Sequence 4, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LESSL, MONIKA
; APPLICANT: PETERS-KOTTIG, MICHAELE
; APPLICANT: BECKMANN, GEORG
; TITLE OF INVENTION: HUMAN MATER PROTEINS
; FILE REFERENCE: SCH-1910
; CURRENT APPLICATION NUMBER: US/10/216,645
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-645-4

Query Match 80.3%; Score 5683.5; DB 14; Length 1143;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1087; Conservative 5; Mismatches 12; Indels 35; Gaps 2;

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Qy          1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60

Qy         61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQ----AMEQEGATAAETEEQ- 115
              |||||||||||||||||||||||||||||||||||||  :    |  :| :  :  |
Db         61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKNSPEDPEATMTDQGPSKEKVPENK 120

Qy        116 ----------------------------EISQAMEQEGATAAETEEQGHGGDTWDYKS 145
                                         ||||||||||||||||||||||||||||||
Db        121 YGMTKLILGVSDISDSNNKHKYVGIHSSFAEISQAMEQEGATAAETEEQGHGGDTWDYKS 180

Qy        146 HVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALAR 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALAR 240

Qy        206 RIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERL 265
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 RIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERL 300

Qy        266 LFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKL 325
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 LFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKL 360

Qy        326 KSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLI 385
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 KSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLI 420

Qy        386 CVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVE 445
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVE 480

Qy        446 GVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYV 505
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYV 540

Qy        506 LEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPV 565
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 LEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPV 600

Qy        566 PLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQN 625
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 PLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQN 660

Qy        626 LDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSML 685
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 LDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSML 720

Qy        686 GTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANR 745
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANR 780

Qy        746 NLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLK 805
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 NLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLK 840

Qy        806 SLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLC 865
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 SLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLC 900

Qy        866 LSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSM 925
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 LSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSM 960

Qy        926 NPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNAL 985
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 NPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNAL 1020

Qy        986 GDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPK 1045
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPK 1080

Qy       1046 GMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDRH 1104
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db       1081 GMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDRY 1139
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RESULT 9
US-10-092-900A-348
; Sequence 348, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.

```
;  APPLICANT:  Ji, Weizhen
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Guo, Xiaojia Sasha
;  APPLICANT:  Tchernev,, Velizar T.
;  APPLICANT:  Fernandes, Elma R.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Liu, Yi
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Leite, Mario W.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Alsobrook, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-290C
;  CURRENT APPLICATION NUMBER: US/10/092,900A
;  CURRENT FILING DATE:  2002-03-07
;  PRIOR APPLICATION NUMBER: USSN 60/274,322
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/283,675
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: USSN 60/338,092
;  PRIOR FILING DATE: 2001-12-03
;  PRIOR APPLICATION NUMBER: USSN 60/274,281
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/274,191
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/325,681
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: USSN 60/304,354
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: USSN 60/279,995
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: USSN 60/294,899
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: USSN 60/287,424
;  PRIOR FILING DATE: 2001-04-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 348
;   LENGTH: 1033
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-092-900A-348

  Query Match             72.3%;  Score 5113.5;  DB 15;  Length 1033;
  Best Local Similarity   95.5%;  Pred. No. 0;
  Matches  976;  Conservative    7;  Mismatches   18;  Indels   21;  Gaps    2;

Qy        104 QEGATAAETEEQEI--SQAMEQEGATAAETEEQG------------------HGGDTWD 142
              :| :|  | : : :   |   || |    : |                  |||||||
Db          8 RETSTLCEPKGRRLRPRQRRNQENVTKNSLKLPGPLQEQTGLGPPHLGSELGLHGGDTWD 67

Qy        143 YKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSA 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 YKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSA 127

Qy        203 LARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRP 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 LARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRP 187

Qy        263 ERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGT 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 ERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGT 247

Qy        323 EKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVG 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 EKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVG 307

Qy        383 SLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRM 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 SLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRM 367

Qy        443 AVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAAL 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 AVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAAL 427

Qy        503 YYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLG 562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 YYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLG 487

Qy        563 CPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPI 622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 CPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPI 547

Qy        623 NQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFC 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 NQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFC 607

Qy        683 SMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVM 742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        608 SMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVM 667

Qy        743 ANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSP 802
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 ANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSP 727

Qy        803 SLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLT 862
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        728 SLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLT 787

Qy        863 HLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLS 922
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        788 HLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLS 847

Qy        923 LSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTD 982
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 LSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTD 907

Qy        983 NALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNF 1042
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 NALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNF 967

Qy       1043 SPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDD 1102
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 SPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDD 1027

Qy       1103 RH 1104
              |:
Db       1028 RY 1029

RESULT 10
US-10-407-866-96
; Sequence 96, Application US/10407866
; Publication No. US20040002593A1
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  APPLICANT:  Godzik, Adam
;  TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
;  TITLE OF INVENTION:  Encoding Nucleic Acids, and Methods of Use
;  FILE REFERENCE: 66654-10(LJ 5755)
;  CURRENT APPLICATION NUMBER: US/10/407,866
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/370,538
;  PRIOR FILING DATE: 2002-04-04
```

```
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
;   LENGTH: 682
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-407-866-96

  Query Match             46.9%;  Score 3318.5;  DB 15;  Length 682;
  Best Local Similarity   93.8%;  Pred. No. 4.9e-274;
  Matches  640;  Conservative    1;  Mismatches    0;  Indels   41;  Gaps    1;

Qy          1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60

Qy         61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKK---------------------- 97
              |||||||||||||||||||||||||||||||||:
Db         61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKRHSPEDPEATMTDQGPSKEKVPGI 120

Qy         98 -----------------ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGD 139
                              |||||||||||||||||||||||||||||||||||||||||||
Db        121 SQAVQQDSATAAETKEQEISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGD 180

Qy        140 TWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIG 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIG 240

Qy        200 KSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIM 259
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIM 300

Qy        260 SRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRD 319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 SRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRD 360

Qy        320 VGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVP 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 VGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVP 420

Qy        380 AVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRF 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRF 480

Qy        440 CRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFC 499
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFC 540

Qy        500 AALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEV 559
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEV 600

Qy        560 LLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVW 619
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 LLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVW 660

Qy        620 LPINQNLDLIASSFCLQHCPYL 641
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Db        661 LPINQNLDLIASSFCLQHCPYL 682


RESULT 11
US-10-216-645-5
; Sequence 5, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
;  APPLICANT: WEISS, BERTRAM
;  APPLICANT:  LESSL, MONIKA
;  APPLICANT:  PETERS-KOTTIG, MICHAELE
;  APPLICANT:  BECKMANN, GEORG
;  TITLE OF INVENTION: HUMAN MATER PROTEINS
;  FILE REFERENCE: SCH-1910
;  CURRENT APPLICATION NUMBER: US/10/216,645
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 1111
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-216-645-5

  Query Match             38.0%;  Score 2688;  DB 14;  Length 1111;
  Best Local Similarity   51.6%;  Pred. No. 8.8e-220;
  Matches  544;  Conservative  183;  Mismatches  281;  Indels   46;  Gaps   10;

Qy         74 TSISIFENMNLRTLSEKARDDMKKISQ------------------AMEQEGATAAETEE 114
              :::|  ||::   | :  ::::: |:                    ||   |    ||
Db         77 STMSPSENVSRAILKDSGSEEVEQASERKMTSPENDSKSIQKDQGPEQEQTSETLQSKEE 136

Qy        115 QEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTL 174
              |:::|           :: :|||  |||:||: ||     |:          | |||: |
Db        137 DEVTEA-----------DKDNGGDLQDYKAHVIAKFDTSVDLH-------YDSPEMKLL 177

Qy        175 AGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQR 234
              : ||   :  |:| |::|||: |:|||||| ||| |||| |:| | |:| |  |||::
Db        178 SDAFKPYQKTFQPHTIILHGRPGVGKSALARSIVLGWAQGKLFQKM-SFVIFFSVREIKW 236

Qy        235 KKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVL-NNDTKLCKDWAEKQ 293
              ::||: : |::| |||   ||:|||:||||||:||| ||: ||| ::|  | :|| ::|
Db        237 TEKSSLAQLIAKECPDSWDLVTKIMSQPERLLFVIDGLDDMDSVLQHDDMTLSRDWKDEQ 296

Qy        294 PPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERG 353
              | : |: ||||| |||:||||:| |: | ||||| |||| |:|| |:|  :|  |:||
Db        297 PIYILMYSLLRKALLPQSFLIITTRNTGLEKLKSMVVSPLYILVEGLSASRRSQLVLENI 356

Qy        354 IGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAF 413
              |  : |   ::: | :| |||| |:| ||:| |||||  :|:      ||||||:|
Db        357 SNESDRIQVFHSLIENHQLFDQCQAPSVCSLVCEALQLQKKLGKRCTLPCQTLTGLYATL 416

Qy        414 VFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALF 473
              |||||| :   :  |: ||:: |   | || |||  :|||  |||    | |||: |||
Db        417 VFHQLTLKRPSQSALSQEEQITLVGLCMMAAEGVWTMRSVFYDDDLKNYSLKESEILALF 476

Qy        474 HMNILLPDSH-CEEYYTFFHLSLQDFCAALYYVLEGL-EIEPALCPLYVEKTKRSMELKQ 531
              ||||||  |  |: | | ||||||| |||||||||| |      |  ::|  :  ||:|:
Db        477 HMNILLQVGHNSEQCYVFSHLSLQDFFAALYYVLEGLEEWNQHFC--FIENQRSIMEVKR 534

Qy        532 AGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGD 591
                  | ||||||||:::|: : ||||   ||   |:||| |||||: || | |:| |
Db        535 TD-DTRLLGMKRFLFGLMNKDILKTLEVLFEYPVIPTVEQKLQHWVSLIAQQVNGTSPMD 593

Qy        592 TLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGI 651
              |||||:||||:||:|||  ||  |||||| ||| :||  ||:||:||  |: ||||:: :
Db        594 TLDAFYCLFESQDEEFVGGALKRFQEVWLLINQKMDLKVSSYCLKHCQNLKAIRVDIRDL 653

Qy        652 FPRDESAEACPVVPLW-MRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLC 710
                | : | |||| :   : | |: | | :|||:||:  :|::|||| |||::|||| ||
Db        654 LSVDNTLELCPVVTVQETQCKPLLMEWWGNFCSVLGSLRNLKELDLGDSILSQRAMKILC 713

Qy        711 AKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALK 770
              :||: :|:|| | |::|::  |::|||::: :|:||: |||| | :|::|:::||||||
Db        714 LELRNQSCRIQKLTFKSAEVVSGLKHLWKLLFSNQNLKYLNLGNTPMKDDDMKLACEALK 773

Qy        771 HPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQ 830
              |||| :|:|||| | ||   |  || :| ::  || |||| |:|  : :: | :||  |
Db        774 HPKCSVETLRLDSCELTIIGYEMISTLLISTTRLKCLSLAKNRVGVKSMISLGNALSSSM 833

Qy        831 CALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSL 890
              | ||||||::||:|   |  | ||| ||::|||||||||||| |||  ||: :| | |:|
Db        834 CLLQKLILDNCGLTPASCHLLVSALFSNQNLTHLCLSNNSLGTEGVQQLCQFLRNPECAL 893

Qy        891 QRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDL 950
              |||:|| |::     ||||: |  |: ||||||:|||| |  :||||| ::||:|:||:|
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Db        894 QRLILNHCNIVDDAYGFLAMRLANNTKLTHLSLTMNPVGDGAMKLLCEALKEPTCYLQEL 953

Qy        951 ELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLK 1010
              ||| | ||  ||| |:|:|: ::||||||| :||||| ||  ||||||| :| | ||||
Db        954 ELVDCQLTQNCCEDLACMITTTKHLKSLDLGNNALGDKGVITLCEGLKQSSSSLRRLGLG 1013

Qy       1011 ACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQ 1070
              || |||:||||||||:||| || |||||:|:||  ||:|||||| || ||| |||||| :
Db       1014 ACKLTSNCCEALSLAISCNPHLNSLNLVKNDFSTSGMLKLCSAFQCPVSNLGIIGLWKQE 1073

Qy       1071 YPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDRH 1104
              |  ::|: ||||: :|| ||||| |:: |||||:
Db       1074 YYARVRRQLEEVEFVKPHVVIDGDWYASDEDDRN 1107


RESULT 12
US-10-399-443-6
; Sequence 6, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute
;  APPLICANT:  Health
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 1111
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-399-443-6

  Query Match             36.4%;  Score 2577;  DB 15;  Length 1111;
  Best Local Similarity   50.8%;  Pred. No. 2.7e-210;
  Matches  535;  Conservative  183;  Mismatches  290;  Indels   46;  Gaps   10;

Qy         74 TSISIFENMNLRTLSEKARDDMKKISQ------------------AMEQEGATAAETEE 114
              :::|  ||::   | :   :::::: |:                  ||   |    ||
Db         77 STMSPSENVSRAILKDSGSEEVEQASERKMTSPENDSKSIQKDQGPEQEQTSETLQSKEE 136

Qy        115 QEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTL 174
               |:::|            :: :|||  |||:||: ||    |:          | |||: |
Db        137 DEVTEA-----------DKDNGGDLQDYKAHVIAKFDTSVDLH-------YDSPEMKLL 177

Qy        175 AGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQR 234
              : ||   :  |:| |::|||: |:|||||| |||  ||| |:| | |:| |  |||::
Db        178 SDAFKPYQKTFQPHTIILHGRPGVGKSALARSIVLGTAQGKLFQKM-SFVIFFSVREIKT 236

Qy        235 KKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVL-NNDTKLCKDWAEKQ 293
              ::||: : |::| |||   ||:|||:||||||:||| ||: ||| ::|  | :|  ::|
Db        237 TEKSSLAQLIAKECPDSTDLVTKIMSQPERLLFVIDGLDDMDSVLQHDDMTLSRDTKDEQ 296

Qy        294 PPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERG 353
              | : |: ||||| |||:||||:| |: | ||||| |||| |:|| |:|  :|  |:||
Db        297 PIYILMYSLLRKALLPQSFLIITTRNTGLEKLKSMVVSPLYILVEGLSASRRSQLVLENI 356

Qy        354 IGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAF 413
              |  : |   ::: | :| |||| |:| ||:| |||||  :|:      ||||||:|
Db        357 SNESDRIQVFHSLIENHQLFDQCQAPSVCSLVCEALQLQKKLGKRCTLPCQTLTGLYATL 416

Qy        414 VFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALF 473
              |||||| :   :  |: ||:: |   | || |||   :|||  |||    | |||: |||

Db        417 VFHQLTLKRPSQSALSQEEQITLVGLCMMAAEGVTTMRSVFYDDDLKNYSLKESEILALF 476

Qy        474 HMNILLPDSH-CEEYYTFFHLSLQDFCAALYYVLEGL-EIEPALCPLYVEKTKRSMELKQ 531
              ||||||   |  |: | | ||||||| |||||||||| |     |  ::|  :  ||:|:
Db        477 HMNILLQVGHNSEQCYVFSHLSLQDFFAALYYVLEGLEETNQHFC--FIENQRSIMEVKR 534

Qy        532 AGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGD 591
                    | ||||||||:::|: : ||||   ||   |:||| | |||: || | |:| |
Db        535 TD-DTRLLGMKRFLFGLMNKDILKTLEVLFEYPVIPTVEQKLQHTVSLIAQQVNGTSPMD 593

Qy        592 TLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGI 651
              |||||:||||:||:|||  ||  |||| | ||| :||  ||:||:||  |: ||||:: :
Db        594 TLDAFYCLFESQDEEFVGGALKRFQEVTLLINQKMDLKVSSYCLKHCQNLKAIRVDIRDL 653

Qy        652 FPRDESAEACPVVPLW-MRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLC 710
              | : | |||| :   : | |: |   :|||:||:  :|::|||| |||::|||| ||
Db        654 LSVDNTLELCPVVTVQETQCKPLLMETTGNFCSVLGSLRNLKELDLGDSILSQRAMKILC 713

Qy        711 AKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALK 770
              :||: :|:|| | |::|::  |::|| ::: :|:||: |||| | :|::|:::||||||
Db        714 LELRNQSCRIQKLTFKSAEVVSGLKHLTKLLFSNQNLKYLNLGNTPMKDDDMKLACEALK 773

Qy        771 HPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQ 830
              |||| :|:|||| | ||   |  || :| ::  || |||| |:|  : :: | :||  |
Db        774 HPKCSVETLRLDSCELTIIGYEMISTLLISTTRLKCLSLAKNRVGVKSMISLGNALSSSM 833

Qy        831 CALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSL 890
              | ||||||::||:|   |  | ||| ||::|||||||||||| |||  ||: :| | |:|
Db        834 CLLQKLILDNCGLTPASCHLLVSALFSNQNLTHLCLSNNSLGTEGVQQLCQFLRNPECAL 893

Qy        891 QRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDL 950
              |||:|| |::     ||||: |  |: ||||||:|||| |  :|||| ::||:|:|:|
Db        894 QRLILNHCNIVDDAYGFLAMRLANNTKLTHLSLTMNPVGDGAMKLLCEALKEPTCYLQEL 953

Qy        951 ELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLK 1010
              ||| | ||  ||| |:|:|: ::||||||| :||||| ||  ||||||| :| | ||||
Db        954 ELVDCQLTQNCCEDLACMITTTKHLKSLDLGNNALGDKGVITLCEGLKQSSSSLRRLGLG 1013

Qy       1011 ACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQ 1070
              || |||:||||||||:||| || |||||:|:||  ||:|||||| || ||| |||| | :
Db       1014 ACKLTSNCCEALSLAISCNPHLNSLNLVKNDFSTSGMLKLCSAFQCPVSNLGIIGLTKQE 1073

Qy       1071 YPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDRH 1104
              |  ::|: ||||: :|| |||||  :: |||||:
Db       1074 YYARVRRQLEEVEFVKPHVVIDGDTYASDEDDRN 1107


RESULT 13
US-10-677-943-6
; Sequence 6, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 1111
;   TYPE: PRT
;   ORGANISM: Mus musculus
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US-10-677-943-6

Query Match 36.4%; Score 2577; DB 15; Length 1111;
Best Local Similarity 50.8%; Pred. No. 2.7e-210;
Matches 535; Conservative 183; Mismatches 290; Indels 46; Gaps 10;

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Qy        74 TSISIFENMNLRTLSEKARDDMKKISQ----------AMEQEGATAAETEE 114
Db        77 STMSPSENVSRAILKDSGSEEVEQASERKMTSPENDSKSIQKDQGPEQEQTSETLQSKEE 136

Qy       115 QEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTL 174
Db       137 DEVTEA----------DKDNGGDLQDYKAHVIAKFDTSVDLH-------YDSPEMKLL 177

Qy       175 AGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQR 234
Db       178 SDAFKPYQKTFQPHTIILHGRPGVGKSALARSIVLGTAQGKLFQKM-SFVIFFSVREIKT 236

Qy       235 KKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVL-NNDTKLCKDWAEKQ 293
Db       237 TEKSSLAQLIAKECPDSTDLVTKIMSQPERLLFVIDGLDDMDSVLQHDDMTLSRDTKDEQ 296

Qy       294 PPFTLIRSLLRKVLLPESPLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERG 353
Db       297 PIYILMYSLLRKALLPQSFLIITTRNTGLEKLKSMVVSPLYILVEGLSASRRSQLVLENI 356

Qy       354 IGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAF 413
Db       357 SNESDRIQVFHSLIENHQLFDQCQAPSVCSLVCEALQLQKKLGKRCTLPCQTLTGLYATL 416

Qy       414 VFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALF 473
Db       417 VFHQLTLKRPSQSALSQEEQITLVGLCMMAAEGVTTMRSVFYDDDLKNYSLKESEILALF 476

Qy       474 HMNILLPDSH-CEEYYTFFHLSLQDFCAALYYVLEGL-EIEPALCPLYVEKTKRSMELKQ 531
Db       477 HMNILLQVGHNSEQCYVFSHLSLQDFFAALYYVLEGLEETNQHFC--FIENQRSIMEVKR 534

Qy       532 AGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGD 591
Db       535 TD-DTRLLGMKRFLFGLMNKDILKTLEVLFEYPVIPTVEQKLQHTVSLIAQQVNGTSPMD 593

Qy       592 TLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGI 651
Db       594 TLDAFYCLFESQDEEFVGGALKRFQEVTLLINQKMDLKVSSYCLKHCQNLKAIRVDIRDL 653

Qy       652 FPRDESAEACPVVPLW-MRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLC 710
Db       654 LSVDNTLELCPVVTVQETQCKPLLMETTGNFCSVLGSLRNLKELDLGDSILSQRAMKILC 713

Qy       711 AKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALK 770
Db       714 LELRNQSCRIQKLTFKSAEVVSGLKHLTKLLFSNQNLKYLNLGNTPMKDDDMKLACEALK 773

Qy       771 HPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQ 830
Db       774 HPKCSVETLRLDSCELTIIGYEMISTLLISTTRLKCLSLAKNRVGVKSMISLGNALSSSM 833

Qy       831 CALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSL 890
Db       834 CLLQKLILDNCGLTPASCHLLVSALFSNQNLTHLCLSNNSLGTEGVQQLCQFLRNPECAL 893

Qy       891 QRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDL 950
Db       894 QRLILNHCNIVDDAYGFLAMRLANNTKLTHLSLTMNPVGDGAMKLLCEALKEPTCYLQEL 953

Qy       951 ELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLK 1010
Db       954 ELVDCQLTQNCCEDLACMITTTKHLKSLDLGNNALGDKGVITLCEGLKQSSSSLRRLGLG 1013

Qy      1011 ACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQ 1070
Db      1014 ACKLTSNCCEALSLAISCNPHLNSLNLVKNDFSTSGMLKLCSAFQCPVSNLGIIGLTKQE 1073

Qy      1071 YPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDRH 1104
Db      1074 YYARVRRQLEEVEFVKPHVVIDGDTYASDEDDRN 1107
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RESULT 14
US-10-399-443-2
; Sequence 2, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-443-2

Query Match 27.4%; Score 1940; DB 15; Length 385;
Best Local Similarity 98.7%; Pred. No. 1.4e-156;
Matches 380; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       252 QAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPES 311
Db         1 QAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDTAEKQPPFTLIRSLLRKVLLPES 60

Qy       312 FLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRE 371
Db        61 FLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRE 120

Qy       372 LLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLE 431
Db       121 LLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLE 180

Qy       432 ERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFF 491
Db       181 ERVVLKRFCRMAVEGVTNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFF 240

Qy       492 HLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSE 551
Db       241 HLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLTMKRFLFGLVSE 300

Qy       552 DVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLA 611
Db       301 DVRRPLEVLLGCPVPLGVKQKLLHTVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLA 360

Qy       612 LNSFQEVWLPINQNLDLIASSFCLQ 636
Db       361 LNSFQEVTLPINQNLDLIASSFCLQ 385
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RESULT 15
US-10-677-943-2
; Sequence 2, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as

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;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 385
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-677-943-2

  Query Match             27.4%;  Score 1940;  DB 15;  Length 385;
  Best Local Similarity   98.7%;  Pred. No. 1.4e-156;
  Matches  380;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        252 QAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPES 311
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db          1 QAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDTAEKQPPFTLIRSLLRKVLLPES 60

Qy        312 FLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRE 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRE 120

Qy        372 LLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLE 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLE 180

Qy        432 ERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFF 491
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 ERVVLKRFCRMAVEGVTNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFF 240

Qy        492 HLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSE 551
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 HLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLTMKRFLFGLVSE 300

Qy        552 DVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLA 611
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        301 DVRRPLEVLLGCPVPLGVKQKLLHTVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLA 360

Qy        612 LNSFQEVWLPINQNLDLIASSFCLQ 636
              ||||||| |||||||||||||||||
Db        361 LNSFQEVTLPINQNLDLIASSFCLQ 385


Search completed: July 19, 2005, 12:19:11
Job time : 479 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 18, 2005, 22:13:46 ; Search time 17004 Seconds
(without alignments)
11498.283 Million cell updates/sec

Title: US-10-066-521-5
Perfect score: 4035
Sequence: 1 atggaaggagacaaatcgct.....tcgaggggctggtgtcttaa 4035

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2917	72.3	3489	6	AX478549	AX478549 Sequence
2	2917	72.3	3885	9	AY154460	AY154460 Homo sapi
3	2917	72.3	3926	6	AX704821	AX704821 Sequence
4	2862	70.9	3830	6	AX704823	AX704823 Sequence
5	2803	69.5	5859	6	AX459881	AX459881 Sequence
6	2803	69.5	6939	6	AX459873	AX459873 Sequence
7	2803	69.5	6939	6	AX459891	AX459891 Sequence
8	2713	67.2	3885	9	AY054986	AY054986 Homo sapi
9	2713	67.2	3900	6	AX427610	AX427610 Sequence
10	1936	48.0	2753	6	CQ731113	CQ731113 Sequence
c 11	1549	38.4	157141	9	AC011470	AC011470 Homo sapi
12	1549	38.4	193609	9	AC024580	AC024580 Homo sapi
13	1102	27.3	1157	6	AX427588	AX427588 Sequence
c 14	900	22.3	167509	2	AC012107	AC012107 Homo sapi
15	657	16.3	1075	6	AX427590	AX427590 Sequence
16	509	12.6	167509	2	AC012107	AC012107 Homo sapi
c 17	219	5.4	164824	2	AC023887	AC023887 Homo sapi
18	174	4.3	164824	2	AC023887	AC023887 Homo sapi
19	165	4.1	1705	9	BC040925	BC040925 Homo sapi
c 20	24	0.6	24	6	AX427600	AX427600 Sequence
c 21	24	0.6	24	6	AX427601	AX427601 Sequence
c 22	23	0.6	439	4	BTOOCORF	Z86039 B.taurus mR
23	23	0.6	3545	4	AY721594	AY721594 Bos tauru
24	23	0.6	159506	9	HS3418	AL021918 Human DNA
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ALIGNMENTS

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LOCUS AX478549 3489 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 3 from Patent WO0248362.
ACCESSION AX478549
VERSION AX478549.1 GI:22217318
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ramkumar,J. and Arvizu,C.
TITLE Embryogenesis associated proteins
JOURNAL Patent: WO 0248362-A 3 20-JUN-2002;
Incyte Genomics, Inc. (US)
FEATURES Location/Qualifiers
source 1. .3489
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Matches 3017; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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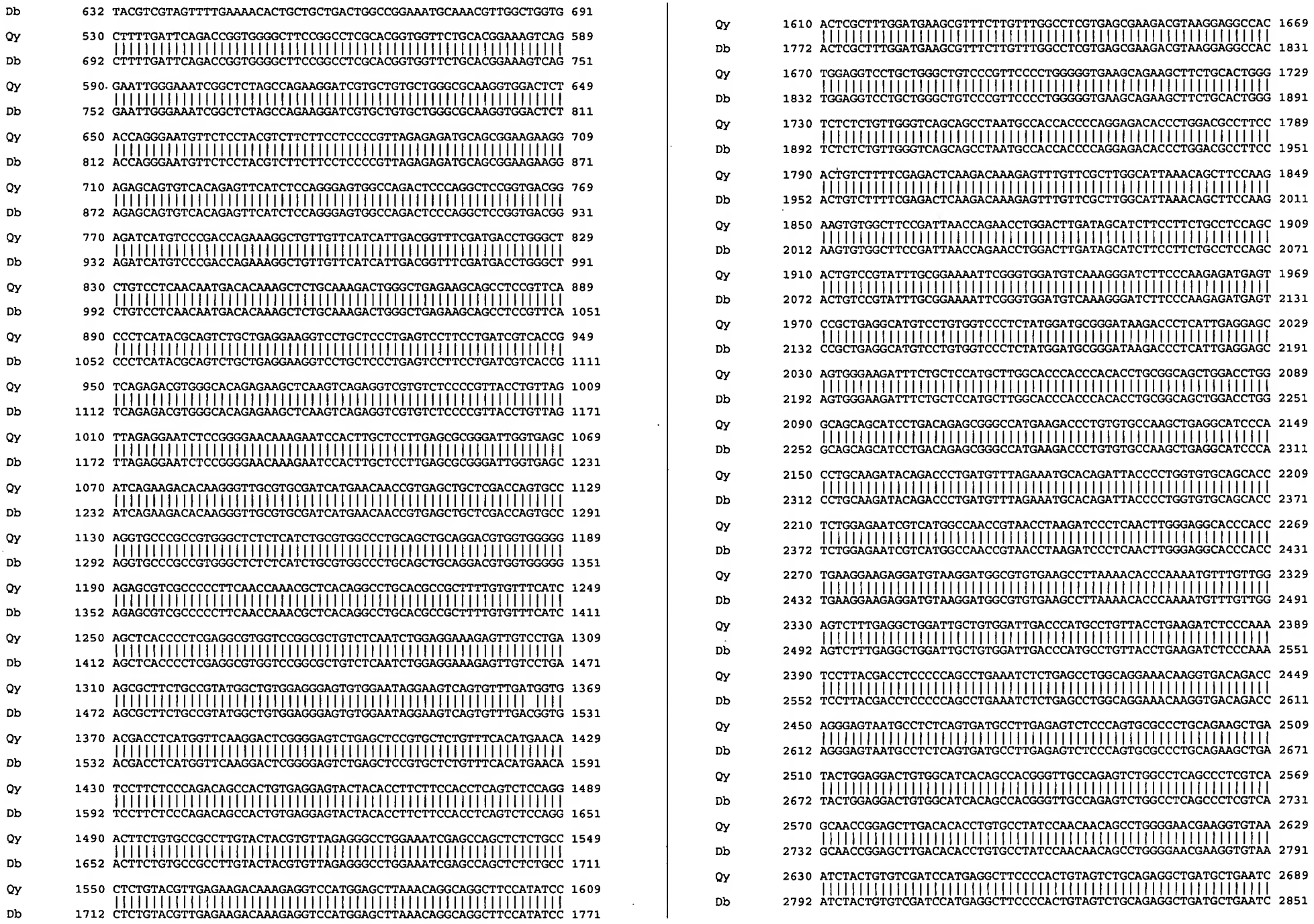
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VERSION AY154460.1 GI:28436363
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ORGANISM Homo sapiens
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REFERENCE 1 (bases 1 to 3885)
AUTHORS Tschopp,J., Martinon,F. and Burns,K.
TITLE NALPs: a novel protein family involved in inflammation
JOURNAL Nat. Rev. Mol. Cell Biol. 4 (2), 95-104 (2003)
MEDLINE 22451042
PUBMED 12563287
REFERENCE 2 (bases 1 to 3885)
AUTHORS Martinon,F., Hofmann,K. and Tschopp,J.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-2002) Institute of Biochemistry, University of Lausanne, ch. des Boveresses 155, Epalinges, VD 1066, Switzerland
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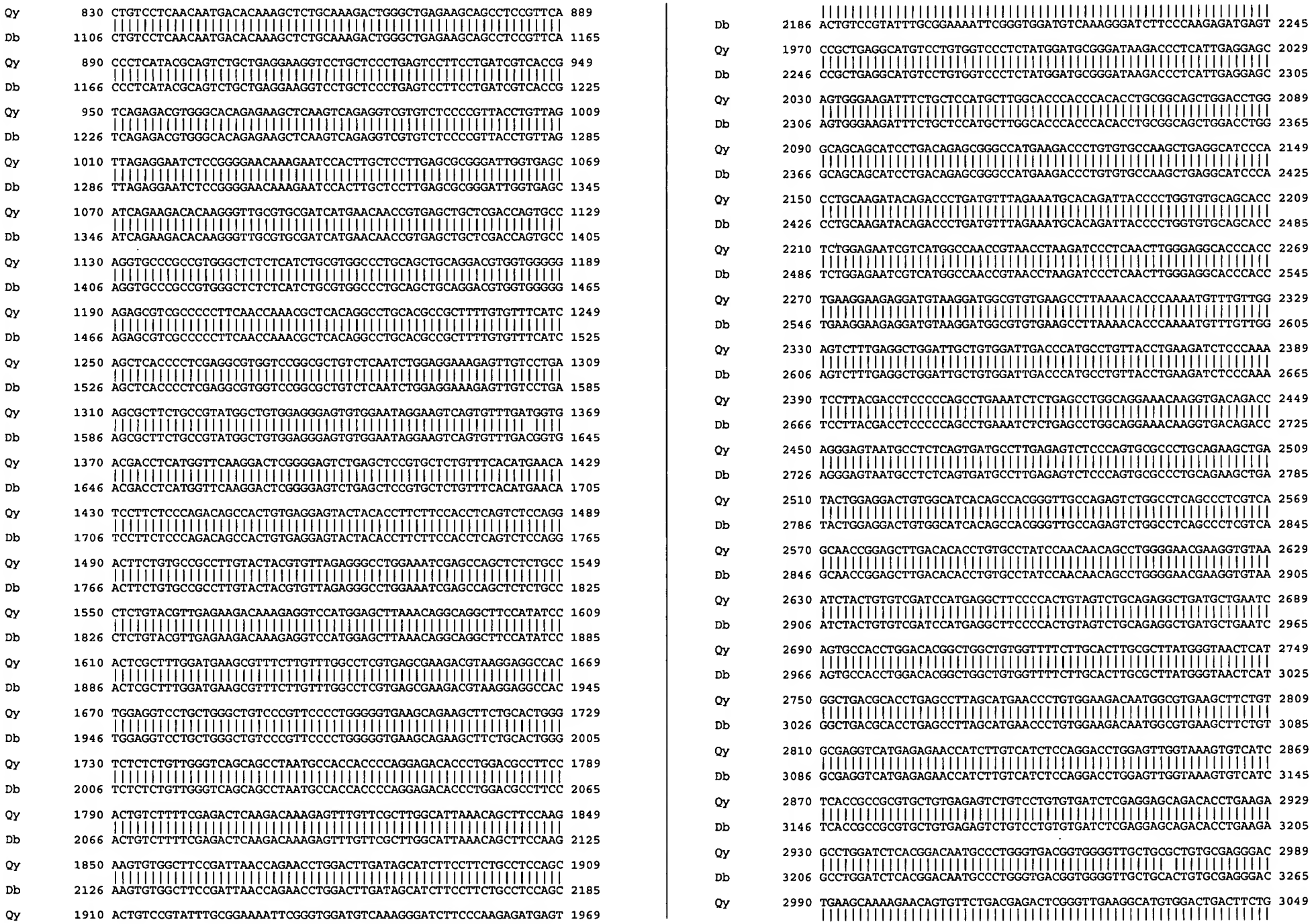
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RESULT 3
AX704821
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DEFINITION  Sequence 1 from Patent EP1285964.
ACCESSION   AX704821
VERSION     AX704821.1  GI:29561487
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Weiss,B., Lessl,M., Peters-Kottig,M. and Beckmann,G.
  TITLE     Human mater proteins
  JOURNAL   Patent: EP 1285964-A 1 26-FEB-2003;
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ORIGIN

  Query Match             72.3%;  Score 2917;  DB 6;  Length 3926;
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  Matches 3017;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy       1190 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1249
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RESULT 4
AX704823
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ACCESSION AX704823
VERSION AX704823.1 GI:29561488
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Weiss,B., Lessl,M., Peters-Kottig,M. and Beckmann,G.
TITLE Human mater proteins
JOURNAL Patent: EP 1285964-A 3 26-FEB-2003;
SCHERING AKTIENGESELLSCHAFT (DE)
FEATURES Location/Qualifiers
source 1. .3830
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ORIGIN

Query Match 70.9%; Score 2862; DB 6; Length 3830;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2962; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION Sequence 24 from Patent WO0240668.
ACCESSION AX459881
VERSION AX459881.1 GI:21725649
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tschopp,J. and Martinon,F.
TITLE Proteins and dna sequences underlying these proteins used for
treating inflammations
JOURNAL Patent: WO 0240668-A 24 23-MAY-2002;
Apotech Research and Development Ltd. (CH)
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Qy       2330 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2389
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Qy       2390 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2449
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Db       4487 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 4546

Qy       2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509
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Qy       2510 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2569
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Qy       2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629
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Qy       2630 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2689
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Db       4727 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 4786

Qy       2690 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 2749
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Db       4787 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 4846

Qy       2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809
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Db       4847 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 4906

Qy       2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869
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Db       4907 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 4966

Qy       2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929
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Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
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Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
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Qy       3110 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3169
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RESULT 6
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DEFINITION  Sequence 16 from Patent WO0240668.
ACCESSION   AX459873
VERSION     AX459873.1  GI:21725645
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tschopp,J. and Martinon,F.
  TITLE     Proteins and dna sequences underlying these proteins used for
            treating inflammations
  JOURNAL   Patent: WO 0240668-A 16 23-MAY-2002;
            Apotech Research and Development Ltd. (CH)
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  Matches 2903;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db       3467 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 3526

Qy        350 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 409
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Qy        410 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 469
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Qy        470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
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Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
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Db       3707 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 3766

Qy        590 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 649
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Db       3767 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 3826

Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
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Db       3887 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 3946

Qy        770 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 829
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Db       3947 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 4006

Qy        830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
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Db       4007 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 4066

Qy        890 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 949
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Db       4067 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 4126

Qy        950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
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Db       4127 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 4186

Qy       1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
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Qy       1070 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 1129
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Db       4247 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 4306

Qy       1130 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1189
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Db       4307 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 4366

Qy       1190 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1249
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Db       4367 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 4426

Qy       1250 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1309
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Qy       1310 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1369
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Db       4547 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 4606

Qy       1430 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1489
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Qy       1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
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Db       4667 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 4726

Qy       1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
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Qy       1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
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Qy       1670 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1729
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Qy       1730 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 1789
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Qy       1790 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 1849
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Qy       1850 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 1909
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Qy       1910 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 1969
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Qy       1970 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2029
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Qy       2030 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2089
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Qy       2090 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2149
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Qy       2150 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2209
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Qy       3170 CCACGTCTAACTTACAGATAATTGG 3194
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RESULT 7
AX459891
LOCUS       AX459891               6939 bp    DNA     linear   PAT 30-NOV-2002
DEFINITION  Sequence 34 from Patent WO0240668.
ACCESSION   AX459891
VERSION     AX459891.1  GI:21725654
KEYWORDS    .
SOURCE      Homo sapiens (human)
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tschopp,J. and Martinon,F.
  TITLE     Proteins and dna sequences underlying these proteins used for
            treating inflammations
  JOURNAL   Patent: WO 0240668-A 34 23-MAY-2002;
            Apotech Research and Development Ltd. (CH)
FEATURES             Location/Qualifiers
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ORIGIN

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Db       3527 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 3586

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Qy        470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
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Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
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Db       3767 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 3826

Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
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Qy        710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
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Qy        770 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 829
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Qy        830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
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RESULT 8
AY054986
LOCUS AY054986 3885 bp mRNA linear PRI 02-APR-2002
DEFINITION Homo sapiens maternal-antigen-that-embryos-require protein (MATER) mRNA, complete cds.
ACCESSION AY054986
VERSION AY054986.1 GI:19882272

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KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3885)
  AUTHORS   Tong,Z.B., Bondy,C.A., Zhou,J. and Nelson,L.M.
  TITLE     A human homologue of mouse Mater, a maternal effect gene essential
            for early embryonic development
  JOURNAL   Hum. Reprod. 17 (4), 903-911 (2002)
  MEDLINE   21922687
   PUBMED   11925379
REFERENCE   2  (bases 1 to 3885)
  AUTHORS   Tong,Z.-B., Bondy,C.A. and Nelson,L.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-AUG-2001) Developmental Endocrinology Branch, NICHD,
            NIH, 10 Center Drive, Bethesda, MD 20892/1862, USA
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ORIGIN

  Query Match           67.2%;  Score 2713;  DB 9;  Length 3885;
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ORIGIN

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3386 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3445

Qy       3170 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3446 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3505

Qy       3230 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3506 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3565

Qy       3290 CTTTTGATGAAGATGACCG 3308
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Db       3566 CTTTTGATGAAGATGACCG 3584
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RESULT 10
CQ731113

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LOCUS       CQ731113                2753 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 17047 from Patent WO02068579.
ACCESSION   CQ731113
VERSION     CQ731113.1  GI:42306827
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 17047 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .2753
                     /organism="Homo sapiens"
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ORIGIN
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Query Match 48.0%; Score 1936; DB 6; Length 2753;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1936; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        404 GACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGG 463
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGG 60

Qy        464 AGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGG 120

Qy        524 CTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAA 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAA 180

Qy        584 AGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTG 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTG 240

Qy        644 GACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGA 300

Qy        704 AGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGG 763
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGG 360

Qy        764 TGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACC 823
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACC 420

Qy        824 TGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTC 883
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTC 480
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Qy        884 CGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCG 943
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Db        481 CGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCG 540

Qy        944 TCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACC 1003
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Db        541 TCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACC 600

Qy       1004 TGTTAGTTAGAGGAATCTCCGGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTG 1063
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGTTAGTTAGAGGAATCTCCGGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTG 660

Qy       1064 GTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACC 1123
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Db        661 GTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACC 720

Qy       1124 AGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGG 1183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGG 780

Qy       1184 TGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGT 1243
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Db        781 TGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGT 840

Qy       1244 TTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTG 1303
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Qy       1304 TCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTG 1363
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Db        901 TCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTG 960

Qy       1364 ATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACA 1423
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Db        961 ATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACA 1020

Qy       1424 TGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTC 1483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTC 1080

Qy       1484 TCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTC 1543
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Db       1081 TCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTC 1140

Qy       1544 TCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCC 1603
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Qy       1604 ATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGA 1663
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Qy       1664 GGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGC 1723
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Qy       1724 ACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACG 1783
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Db       1321 ACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACG 1380

Qy       1784 CCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCT 1843
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Db       1381 CCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCT 1440

Qy       1844 TCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCC 1903
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Qy       1904 TCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAG 1963
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Db       1501 TCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAG 1560

Qy       1964 ATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTG 2023
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTG 1620

Qy       2024 AGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGG 2083
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGG 1680

Qy       2084 ACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGC 2143
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Qy       2144 ATCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGC 2203
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Qy       2204 AGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCA 2263
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Db       1801 AGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCA 1860

Qy       2264 CCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTT 2323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTT 1920

Qy       2324 TGTTGGAGTCTTTGAG 2339
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RESULT 11
AC011470/c
LOCUS       AC011470              157141 bp    DNA     linear   PRI 15-JUL-2000
DEFINITION  Homo sapiens chromosome 19 clone CTC-490M10, complete sequence.
ACCESSION   AC011470
VERSION     AC011470.5  GI:9211204
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 157141)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 157141)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 157141)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jul 15, 2000 this sequence version replaced gi:7690109.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.9% of Sequence;
            Estimated Total Number of Errors is 0.1.
FEATURES             Location/Qualifiers
     source          1. .157141
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="19"
                     /clone="CTC-490M10"
ORIGIN

  Query Match           38.4%;  Score 1549;  DB 9;  Length 157141;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1599;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy        402 AGGACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGA 461
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Db      42001 AGGACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGA 41942

Qy        462 GGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTT 521
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Db      41941 GGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTT 41882

Qy        522 GGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGG 581
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Db      41881 GGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGG 41822

Qy        582 AAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGG 641
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Db      41821 AAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGG 41762

Qy        642 TGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCG 701
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Db      41761 TGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCG 41702

Qy        702 GAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCC 761
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Db      41701 GAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCC 41642

Qy        762 GGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGA 821
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41641 GGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGA 41582

Qy        822 CCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCC 881
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        882 TCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGAT 941
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41521 TCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGAT 41462

Qy        942 CGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTA 1001
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41461 CGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTA 41402

Qy       1002 CCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGAT 1061
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Db      41401 CCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGAT 41342

Qy       1062 TGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGA 1121
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Db      41341 TGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGA 41282

Qy       1122 CCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGT 1181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41281 CCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGT 41222

Qy       1182 GGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGT 1241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41221 GGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGT 41162

Qy       1242 GTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGT 1301
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Db      41161 GTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGT 41102

Qy       1302 TGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTT 1361
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Qy       1362 TGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCA 1421
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41041 TGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCA 40982

Qy       1422 CATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAG 1481
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Db      40981 CATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAG 40922

Qy       1482 TCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGC 1541
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Db      40921 TCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGC 40862

Qy       1542 TCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTT 1601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40861 TCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTT 40802

Qy       1602 CCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAG 1661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40801 CCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAG 40742

Qy       1662 GAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCT 1721
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40741 GAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCT 40682

Qy       1722 GCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGA 1781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40681 GCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGA 40622

Qy       1782 CGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAG 1841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40621 CGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAG 40562

Qy       1842 CTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTG 1901
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Db      40561 CTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTG 40502

Qy       1902 CCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAG 1961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      40501 CCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAG 40442

Qy       1962 AGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGG 2001
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Db      40441 AGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGG 40402
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RESULT 12
AC024580
LOCUS       AC024580              193609 bp    DNA     linear   PRI 21-DEC-2001
DEFINITION  Homo sapiens chromosome 19 clone CTD-2621I17, complete sequence.
ACCESSION   AC024580
VERSION     AC024580.6  GI:17975240
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 193609)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 193609)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 193609)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 193609)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Dec 21, 2001 this sequence version replaced gi:16905144.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.4% of Sequence;
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FEATURES             Location/Qualifiers
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ORIGIN

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Qy        402 AGGACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGA 461
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Db      22257 AGGACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGA 22316

Qy        462 GGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTT 521
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Db      22317 GGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTT 22376

Qy        522 GGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGG 581
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Db      22377 GGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGG 22436

Qy        582 AAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGG 641
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Db      22437 AAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGG 22496

Qy        642 TGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCG 701
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Qy        762 GGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGA 821
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Qy        822 CCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCC 881
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Qy        882 TCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGAT 941
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Qy        942 CGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTA 1001
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Qy       1002 CCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGAT 1061
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Db      22857 CCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGAT 22916

Qy       1062 TGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGA 1121
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Db      22917 TGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGA 22976

Qy       1122 CCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGT 1181
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Qy       1242 GTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGT 1301
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Qy       1302 TGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTT 1361
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Qy       1422 CATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAG 1481
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Qy       1542 TCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTT 1601
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Qy       1602 CCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAG 1661
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Qy       1662 GAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCT 1721
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Db      23637 CGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAG 23696

Qy       1842 CTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTG 1901
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Db      23697 CTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTG 23756

Qy       1902 CCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAG 1961
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Db      23757 CCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAG 23816

Qy       1962 AGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGG 2001
              |||||||||||||||||||||||||||||||||||||||
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RESULT 13
AX427588
LOCUS       AX427588               1157 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 1 from Patent WO0232955.
ACCESSION   AX427588
VERSION     AX427588.1  GI:21537711
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nelson,L.M. and Tong,Z.-B.
  TITLE     Human gene critical to fertility
  JOURNAL   Patent: WO 0232955-A 1 25-APR-2002;
            GOVERNMENT OF THE UNITED STATES (US)
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  Matches 1152;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy        817 GATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 876
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Db         64 GATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 123

Qy        877 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 936
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Db        124 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 183

Qy        937 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 996
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Db        184 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 243

Qy        997 CGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGC 1056
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Db        244 CGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGC 303

Qy       1057 GGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTG 1116
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Db        304 GGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTG 363

Qy       1117 CTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAG 1176
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Db        364 CTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAG 423

Qy       1177 GACGTGGTGGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCT 1236
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Qy       1297 AGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCA 1356
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Qy       1357 GTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTG 1416
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Qy       1417 TTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCAC 1476
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Qy       1477 CTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAG 1536
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Qy       1537 CCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCA 1596
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Db        784 CCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCA 843

Qy       1597 GGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGAC 1656
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Qy       1657 GTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAG 1716
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Qy       1717 CTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACC 1776
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Qy       1777 CTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTA 1836
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Qy       1897 TTCTGCCTCCAGC 1909
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RESULT 14
AC012107/c
LOCUS       AC012107               167509 bp    DNA     linear   HTG 28-MAR-2000
DEFINITION  Homo sapiens clone RP11-45K21, WORKING DRAFT SEQUENCE, 25 unordered
            pieces.
ACCESSION   AC012107
VERSION     AC012107.2  GI:7329252
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 167509)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-45K21
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 167509)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
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            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 26, 2000 this sequence version replaced gi:6088020.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L1180
                Center clone name: 45_K_21
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-primer-amersham; 4% of reads
                Chemistry: Dye-terminator Big Dye; 96% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 145437 bases at least Q40
                Consensus quality: 155496 bases at least Q30
                Consensus quality: 159832 bases at least Q20
                Insert size: 176000; agarose-fp
                Insert size: 165109; sum-of-contigs
                Quality coverage: 3.8 in Q20 bases; agarose-fp
                Quality coverage: 4.1 in Q20 base.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 25 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
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            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
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            * be preserved.
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            *     1062     1161: gap of 100 bp
            *     1162     2381: contig of 1220 bp in length
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            *     3772     3871: gap of 100 bp
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RESULT 15
AX427590
LOCUS       AX427590               1075 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 3 from Patent WO0232955.
ACCESSION   AX427590
VERSION     AX427590.1  GI:21537712
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nelson,L.M. and Tong,Z.-B.
  TITLE     Human gene critical to fertility
  JOURNAL   Patent: WO 0232955-A 3 25-APR-2002;
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             16.3%;  Score 657;  DB 6;  Length 1075;
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Job time : 17013 secs
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GenCore version 5.1.6

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Run on: July 18, 2005, 17:31:03 ; Search time 2009 Seconds
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	2917	72.3	3489	6	AAD41224	Aad41224 Human EMB
	4	2917	72.3	3926	8	ADA45218	Ada45218 Human MAT
	5	2862	70.9	3830	8	ADA45220	Ada45220 Human MAT
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	26	22	0.5	26	8	AAD49004	Aad49004 Human MAT
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	36	21	0.5	21	6	ABK48624	Abk48624 Human MAT
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ALIGNMENTS

RESULT 1
AAL44356
ID AAL44356 standard; cDNA; 4035 BP.
XX
AC AAL44356;
XX
DT 31-OCT-2002 (first entry)
XX
DE Human PYRIN-5 cDNA sequence.
XX
KW Human; gene; ss; gene therapy; PYRIN; stress-related response;
KW apoptopic response; inflammatory response; inflammatory disorder;
KW immune system disorder; Crohn's disease; multiple sclerosis; cancer;
KW leukaemia; autoimmune disorder; arthritis; neurological disease;
KW Alzheimer's disease; Parkinson's disease; chromosomal mapping;
KW tissue typing; forensic biology; predictive medicine; pharmacogenomics;
KW transcription profiling; PYRIN-5.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .4035
FT /*tag= a
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XX
PN WO200261049-A2.
XX
PD 08-AUG-2002.
XX
PF 31-JAN-2002; 2002WO-US002967.
XX
PR 31-JAN-2001; 2001US-0265231P.
PR 10-SEP-2001; 2001US-0318645P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
PA (AMHP) WYETH.
XX
PI Bertin J, Wang W, Blatcher M;
XX
DR WPI; 2002-627477/67.
DR P-PSDB; AAO15585.
XX
PT New PYRIN polypeptides and nucleic acids useful for modulating and

PT diagnosing stress-related, apoptopic and inflammatory responses, or for
PT treating inflammatory and immune system disorders, cancers, or
PT neurological diseases.
XX
PS Claim 4; Fig 3; 167pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human
CC PYRIN proteins. The PYRIN protein and DNA sequences of the invention are
CC useful for modulating and diagnosing stress-related, apoptopic and
CC inflammatory responses. The PYRIN protein and DNA sequences are useful
CC for treating: inflammatory disorders and immune system disorders (e.g.
CC Crohn's disease, reactive arthritis, multiple sclerosis, contact
CC dermatitis, psoriasis, graft rejection, allergies, viral infections and
CC bacterial infections); cancer (e.g. leukaemia); autoimmune disorders
CC (e.g. systemic lupus erythematosus and arthritis); and neurological
CC diseases (e.g. Alzheimer's disease and Parkinson's disease). The PYRIN
CC protein and DNA sequences may also be used in screening assays, detection
CC assays (e.g. chromosomal mapping, tissue typing or forensic biology),
CC predictive medicine (e.g. diagnostic assays, clinical trials and
CC pharmacogenomics) and transcription profiling. The present DNA sequence
CC encodes the human PYRIN-5 protein
XX
SQ Sequence 4035 BP; 935 A; 1022 C; 1175 G; 903 T; 0 U; 0 Other;

Query Match 100.0%; Score 4035; DB 6; Length 4035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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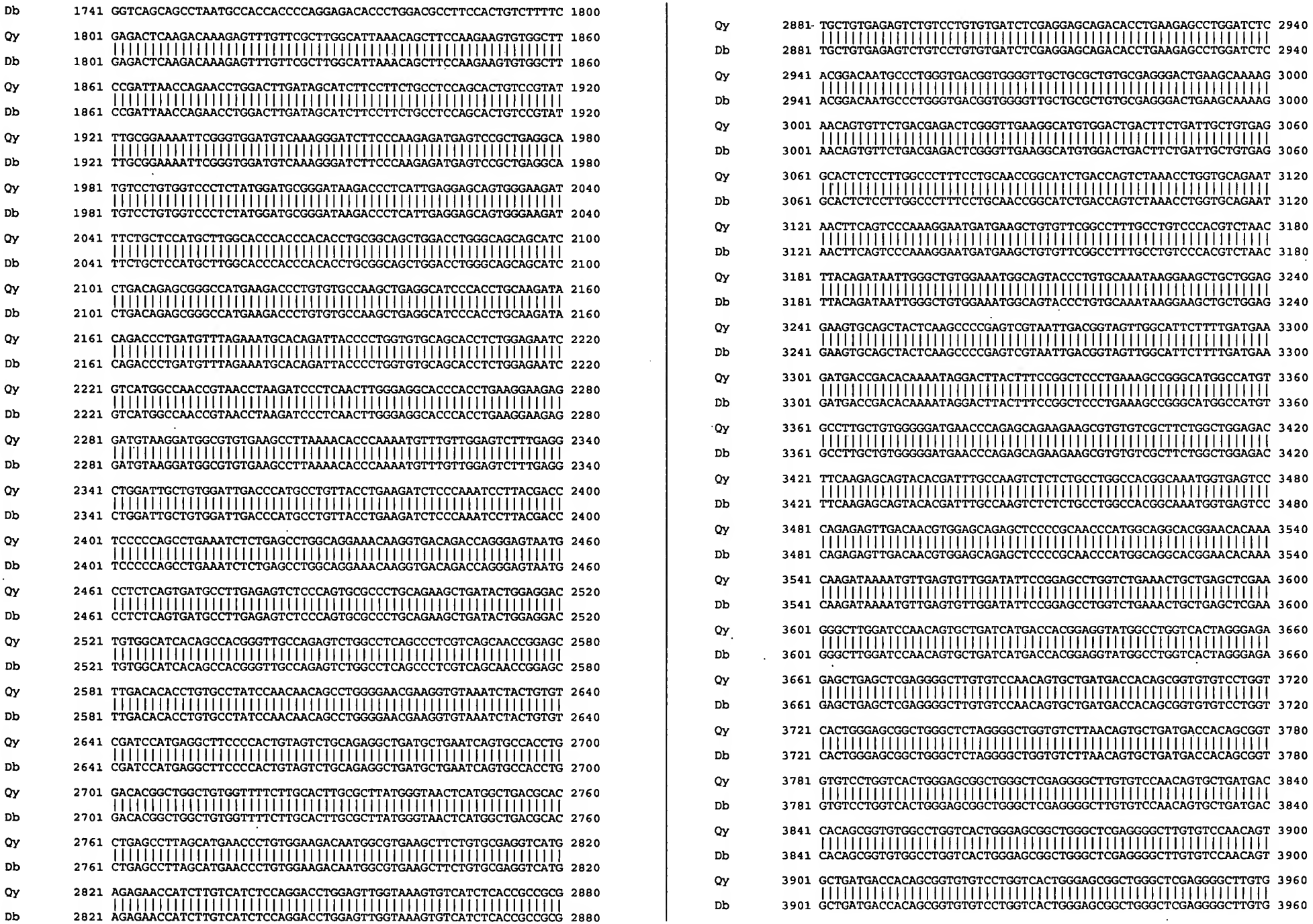
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RESULT 2
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ID   ADF94744 standard; cDNA; 4035 BP.
XX
AC   ADF94744;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human PYRIN-5 coding sequence.
XX
KW   human; PYRIN; inflammatory disorder; inappropriate apoptosis;
KW   inflammatory bowel disease; rheumatoid arthritis; diabetes;
KW   multiple sclerosis; Grave's disease; contact dermatitis; psoriasis;
KW   graft rejection; asthma; allergy; chronic obstructive pulmonary disease;
KW   glomerulonephritis; infection; Alzheimer's disease; Parkinson's disease;
KW   anaemia; ischaemia; screening; chromosomal mapping; tissue typing;
KW   forensic biology; pharmacogenomics; predictive medicine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003089588-A2.
XX
PD   30-OCT-2003.
XX
PF   14-APR-2003; 2003WO-US011572.
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PR   17-APR-2002; 2002US-00124498.
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XX
PI   Bertin J,  Wang W,  Blatcher M;
XX
DR   WPI; 2003-845527/78.
DR   P-PSDB; ADF94745.
XX
PT   New nucleic acid molecules and polypeptides (e.g. PYRIN-2 or PYRIN-3)
PT   useful for diagnosing, preventing or treating inflammation or disorders
PT   associated with inappropriate apoptosis, in chromosomal mapping or in
PT   pharmacogenomics.
XX
PS   Claim 4; SEQ ID NO 5; 199pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of human
CC   PYRIN proteins. The DNA and protein sequences of the invention are useful
CC   in diagnosing, preventing and treating inflammatory disorders or
CC   disorders associated with inappropriate apoptosis, such as: inflammatory
CC   bowel disease, rheumatoid arthritis, diabetes, multiple sclerosis,
CC   Grave's disease, contact dermatitis, psoriasis, graft rejection, asthma,
CC   allergy, chronic obstructive pulmonary disease, glomerulonephritis,
CC   infections, Alzheimer's disease, Parkinson's disease, anaemia and
CC   ischaemia. The DNA and protein sequences of the invention may also be
CC   used in screening assays, chromosomal mapping, tissue typing, forensic
CC   biology, pharmacogenomics, predictive medicine, and in monitoring of
CC   clinical trials. The present DNA sequence encodes a PYRIN protein of the
CC   invention.
XX
SQ   Sequence 4035 BP; 935 A; 1022 C; 1175 G; 903 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 4035;  DB 10;  Length 4035;
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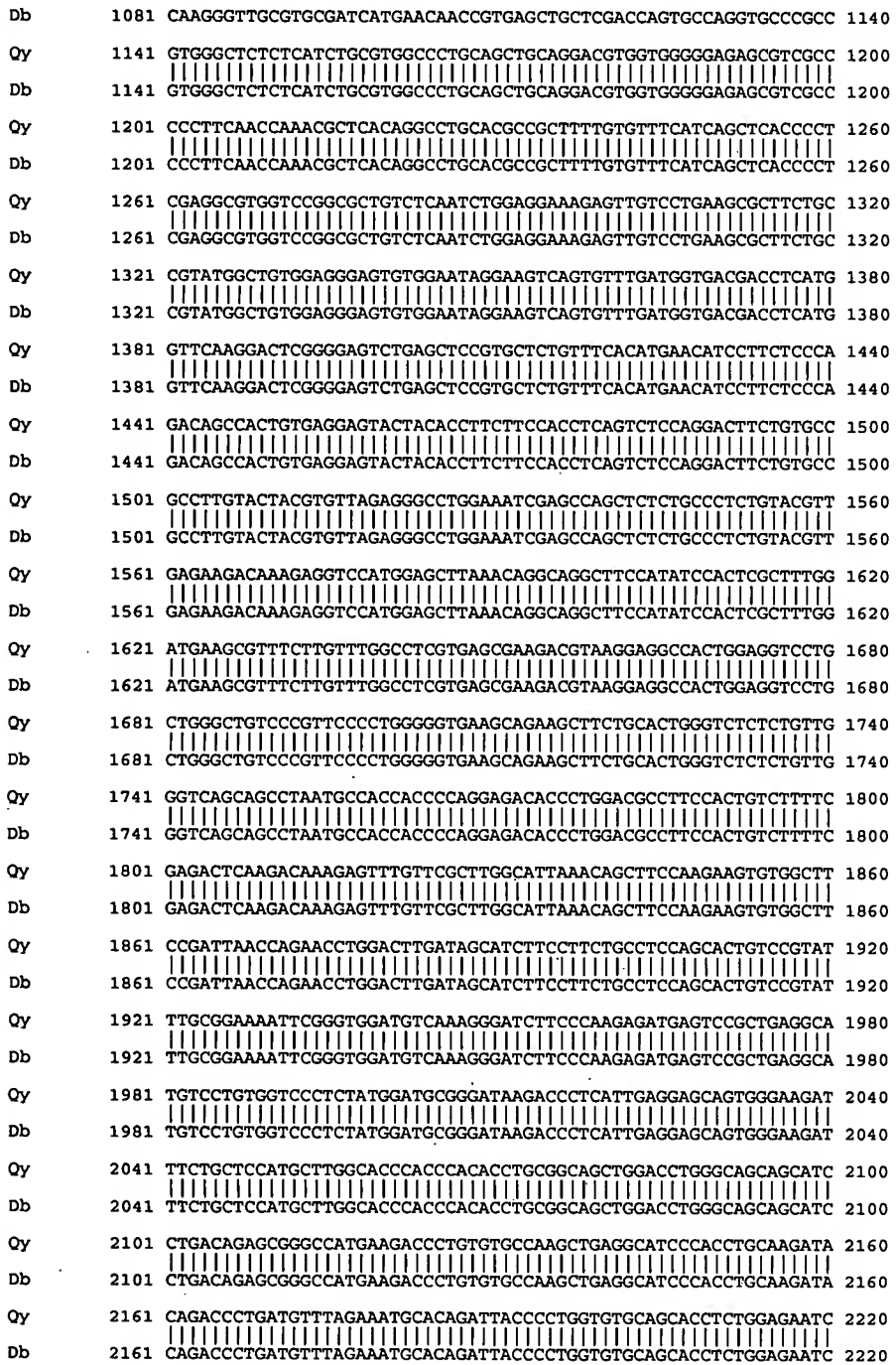
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Db 2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Qy 2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Db 2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Qy 2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Db 2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Qy 2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
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Db 2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
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Db 2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
Qy 3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Db 3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Qy 3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
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Qy       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360

Qy       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
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Qy       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
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Db       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540

Qy       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660

Qy       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
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Qy       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
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Db       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780

Qy       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
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Db       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840

Qy       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960

Qy       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020

Qy       4021 GGGCTGGTGTCTTAA 4035
             |||||||||||||||
Db       4021 GGGCTGGTGTCTTAA 4035
```

```
RESULT 3
AAD41224
ID   AAD41224 standard; cDNA; 3489 BP.
XX
AC   AAD41224;
XX
DT   30-OCT-2002  (first entry)
XX
DE   Human EMBRY-1 cDNA.
XX
KW   Human; embryogenesis associated protein; AIDS; reproductive disorder;
KW   infertility; endometriosis; endometrial tumour; inflammatory disorder;
KW   autoimmune disorder; acquired immune deficiency syndrome; transgenic;
KW   ovarian tumour; contact dermatitis; placenta disorder; preeclampsia;
KW   EMBRY-1; allergy; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3489
FT                   /*tag=  a
FT                   /product= "EMBRY-1 protein"
XX
PN   WO200248362-A2.
XX
PD   20-JUN-2002.
XX
PF   14-NOV-2001; 2001WO-US043956.
XX
PR   15-NOV-2000; 2000US-0249407P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Ramkumar J,  Arvizu C;
XX
DR   WPI; 2002-537629/57.
DR   P-PSDB; AAE25053.
XX
PT   New polypeptides of human embryogenesis associated proteins for screening
PT   modulators useful for treating or preventing disorders e.g.
PT   endometriosis, infertility, allergy, preeclampsia.
XX
PS   Claim 58; Page 95-96; 97pp; English.
XX
CC   The invention relates to human embryogenesis associated proteins (EMBRY)
CC   and nucleic acid molecules encoding such proteins. EMBRY sequences are
CC   useful for screening modulators useful for treating or preventing
CC   disorders associated with abnormal expression of EMBRY. The disorders
CC   treated include reproductive disorders such as infertility,
CC   endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory
CC   disorder such as acquired immune deficiency syndrome (AIDS), allergies,
CC   contact dermatitis; disorders of the placenta such as preeclampsia,
CC   abruptio placentae etc. Sequences of the invention are also useful for
CC   analysing a proteome of a tissue or a cell type. EMBRY proteins are
CC   useful as immunogens for preparing antibodies. Polynucleotides of the
CC   invention are useful for creating knockin humanised animals or transgenic
CC   animals to model human diseases. They are also used in gene therapy. The
CC   present sequence is human EMBRY-1 cDNA
XX
SQ   Sequence 3489 BP; 854 A; 881 C; 961 G; 793 T; 0 U; 0 Other;
```

```
  Query Match             72.3%;  Score 2917;  DB 6;  Length 3489;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3017;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 511

Qy        350 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 571

Qy        410 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 631

Qy        470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 691

Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 751

Qy        590 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 649
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Db        752 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 811

Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
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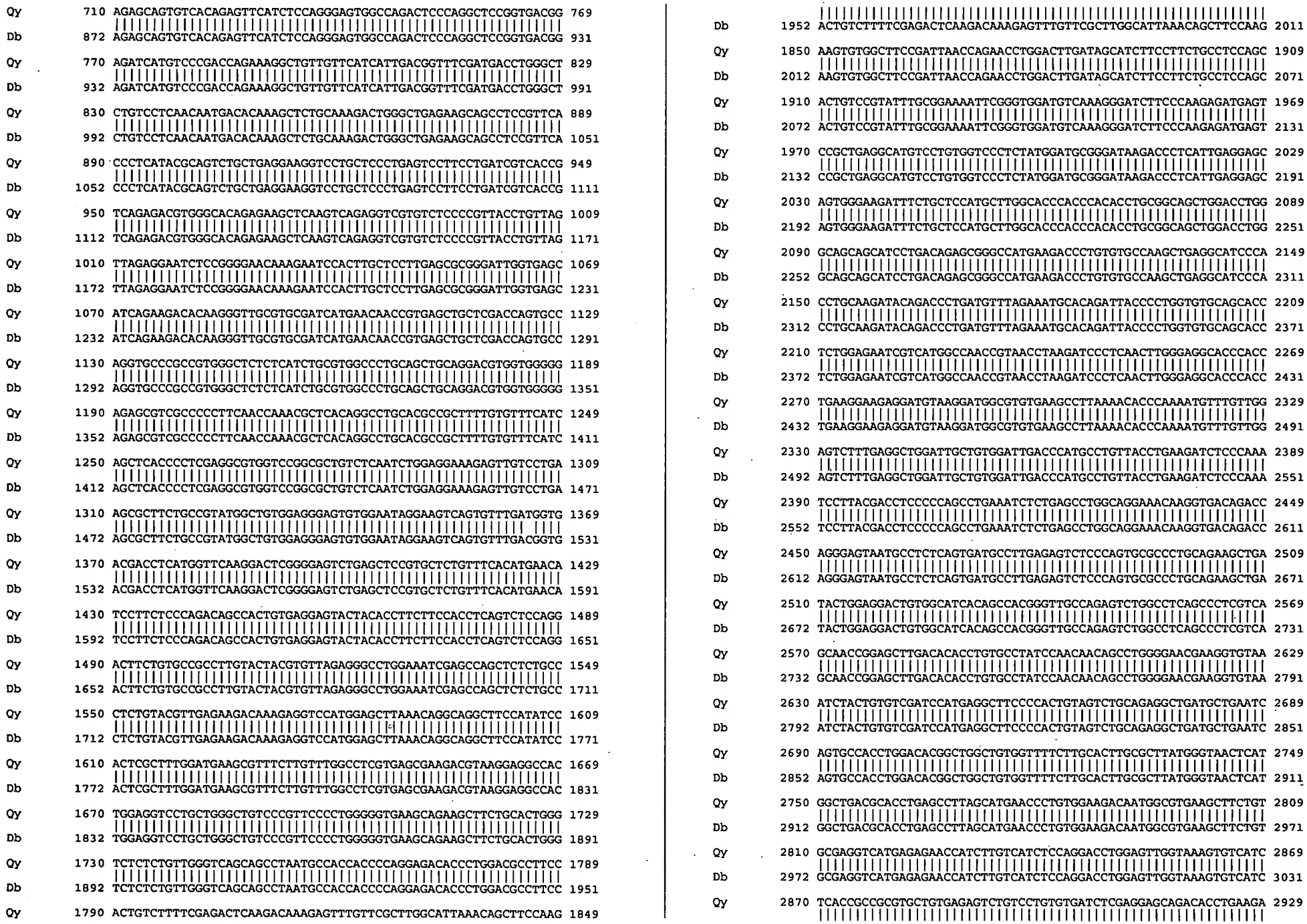
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Db 932 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 991
Qy 830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
Db 992 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 1051
Qy 890 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 949
Db 1052 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 1111
Qy 950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
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Qy 1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
Db 1172 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1231
Qy 1070 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 1129
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Qy 1190 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1249
Db 1352 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1411
Qy 1250 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1309
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Qy 1310 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1369
Db 1472 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTG 1531
Qy 1370 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1429
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Qy 1430 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1489
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Qy 1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
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Qy 1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
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Qy 1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
Db 1772 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1831
Qy 1670 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1729
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Qy 2090 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2149
Db 2252 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2311
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Db 2312 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2371
Qy 2210 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2269
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Qy 2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509
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Qy 2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629
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Db       3032 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 3091

Qy       2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       3092 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGAC 3151

Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3152 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3211

Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
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Db       3212 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3271

Qy       3110 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3272 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3331

Qy       3170 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3229
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Db       3332 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3391

Qy       3230 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3392 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3451

Qy       3290 CTTTTGATGAAGATGACCG 3308
             ||||||||||||||||||
Db       3452 CTTTTGATGAAGATGACCG 3470
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```
RESULT 4
ADA45218
ID   ADA45218 standard; DNA; 3926 BP.
XX
AC   ADA45218;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MATER DNA.
XX
KW   human ; MATER; maternal antigen that embryos require; NTP-ase;
KW   nucleoside triphosphate-ase; apoptosis; antiinfertility; contraceptive;
KW   antiinflammatory; immunosuppressive; gynaecological; endometriosis;
KW   ovarian dysfunction; autoimmune premature ovarian failure;
KW   autoimmune disease; contraceptive; autoantibody; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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XX
PN   EP1285964-A2.
XX
PD   26-FEB-2003.
XX
PF   12-JUL-2002; 2002EP-00090246.
XX
PR   10-AUG-2001; 2001DE-01039874.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Weiss B,  Lessl M,  Peters-Kottig M,  Beckmann G;
XX
DR   WPI; 2003-302814/30.
DR   P-PSDB; ADA45219.
XX
PT   New nucleic acid for human maternal antigen that embryos require protein,
PT   useful e.g. in diagnosis and treatment of female infertility.
XX
PS   Claim 1; Page 9-11; 31pp; German.
XX
CC   This invention describes a novel human MATER (maternal antigen that
CC   embryos require) protein. MATER is an NTP(nucleoside triphosphate)-ase
CC   associated with apoptosis, a defect in MATER activity causes growth
CC   arrest at the 2-cell stage of fertilized eggs. mRNA transcribed from the
CC   MATER gene is found predominantly in ovary, testis and placenta. The
CC   products of the invention have antiinfertility, contraceptive,
CC   antiinflammatory, immunosuppressive and gynaecological activity.
CC   Effectors of the MATER polypeptide are used to treat infertility
CC   associated with endometriosis and also ovarian dysfunction, autoimmune
CC   premature ovarian failure, inflammation, autoimmune diseases and female
CC   infertility, and as contraceptives. Measurements of autoantibodies
CC   against MATER in body samples or MATER protein or mRNA in eggs is useful
CC   for diagnosis of female infertility, particularly by detecting mutations
CC   in the MATER gene with a DNA chip. This sequence encodes the human MATER
CC   polypeptide described in the invention.
XX
SQ   Sequence 3926 BP; 969 A; 958 C; 1061 G; 938 T; 0 U; 0 Other;

  Query Match             72.3%;  Score 2917;  DB 8;  Length 3926;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3017;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        290 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 511

Qy        350 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 571

Qy        410 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 631

Qy        470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 691

Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 751

Qy        590 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 811

Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 871

Qy        710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 931

Qy        770 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 991

Qy        830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        992 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 1051

Qy        890 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1052 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 1111

Qy        950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1112 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1171

Qy       1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1172 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1231

Qy       1070 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 1129
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1232 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 1291

Qy       1130 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1292 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1351

Qy       1190 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1352 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1411

Qy       1250 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1412 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1471

Qy       1310 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       1472 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTG 1531

Qy       1370 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1532 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1591

Qy       1430 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1592 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1651

Qy       1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1652 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1711

Qy       1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1712 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1771

Qy       1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1772 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1831

Qy       1670 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1832 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1891

Qy       1730 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 1789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1892 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 1951

Qy       1790 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 1849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1952 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 2011

Qy       1850 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 1909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2012 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 2071

Qy       1910 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 1969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2072 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 2131

Qy       1970 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2132 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2191

Qy       2030 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2192 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2251

Qy       2090 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2252 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2311

Qy       2150 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2312 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2371

Qy       2210 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2372 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2431

Qy       2270 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2432 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2491

Qy       2330 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2492 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2551

Qy       2390 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2552 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2611

Qy       2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2612 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2671

Qy       2510 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2672 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2731

Qy       2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2732 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2791

Qy       2630 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2792 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2851

Qy       2690 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 2749
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Db       2852 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 2911

Qy       2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2912 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2971

Qy       2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2972 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 3031

Qy       2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3032 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 3091

Qy       2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       3092 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGAC 3151

Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3152 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3211

Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3212 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3271

Qy       3110 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3272 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3331

Qy       3170 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3332 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3391
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Qy       3230 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3392 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3451

Qy       3290 CTTTTGATGAAGATGACCG 3308
             ||||||||||||||||||||
Db       3452 CTTTTGATGAAGATGACCG 3470


RESULT 5
ADA45220
ID   ADA45220 standard; DNA; 3830 BP.
XX
AC   ADA45220;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MATER splice variant DNA SEQ ID 3.
XX
KW   human; MATER; maternal antigen that embryos require; NTP-ase;
KW   nucleoside triphosphate-ase; apoptosis; antiinfertility; contraceptive;
KW   antiinflammatory; immunosuppressive; gynaecological; endometriosis;
KW   ovarian dysfunction; autoimmune premature ovarian failure;
KW   autoimmune disease; contraceptive; autoantibody; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3432
FT                   /*tag=  a
FT                   /product= "splice variant of MATER"
XX
PN   EP1285964-A2.
XX
PD   26-FEB-2003.
XX
PF   12-JUL-2002; 2002EP-00090246.
XX
PR   10-AUG-2001; 2001DE-01039874.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Weiss B,  Lessl M,  Peters-Kottig M,  Beckmann G;
XX
DR   WPI; 2003-302814/30.
DR   P-PSDB; ADA45221.
XX
PT   New nucleic acid for human maternal antigen that embryos require protein,
PT   useful e.g. in diagnosis and treatment of female infertility.
XX
PS   Claim 1; Page 17-18; 31pp; German.
XX
CC   This invention describes a novel human MATER (maternal antigen that
CC   embryos require) protein. MATER is an NTP(nucleoside triphosphate)-ase
CC   associated with apoptosis, a defect in MATER activity causes growth
CC   arrest at the 2-cell stage of fertilized eggs. mRNA transcribed from the
CC   MATER gene is found predominantly in ovary, testis and placenta. The
CC   products of the invention have antiinfertility, contraceptive,
CC   antiinflammatory, immunosuppressive and gynaecological activity.
CC   Effectors of the MATER polypeptide are used to treat infertility
CC   associated with endometriosis and also ovarian dysfunction, autoimmune
CC   premature ovarian failure, inflammation, autoimmune diseases and female
CC   infertility, and as contraceptives. Measurements of autoantibodies
CC   against MATER in body samples or MATER protein or mRNA in eggs is useful
CC   for diagnosis of female infertility, particularly by detecting mutations
CC   in the MATER gene with a DNA chip. This sequence represents a splice
CC   variant of human MATER in which exon 4 of the usual form is absent.
XX
SQ   Sequence 3830 BP; 943 A; 946 C; 1041 G; 900 T; 0 U; 0 Other;

  Query Match             70.9%;  Score 2862;  DB 8;  Length 3830;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2962;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        345 AGAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGG 404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 AGAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGG 509

Qy        405 ACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGA 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 ACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGA 569

Qy        465 GGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGC 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 GGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGC 629

Qy        525 TGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAA 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 TGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAA 689

Qy        585 GTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGG 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGG 749

Qy        645 ACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAA 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 ACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAA 809

Qy        705 GAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGT 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 GAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGT 869

Qy        765 GACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCT 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 GACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCT 929

Qy        825 GGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCC 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        930 GGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCC 989

Qy        885 GTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGT 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 GTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGT 1049

Qy        945 CACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCT 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 CACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCT 1109

Qy       1005 GTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGG 1064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1110 GTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGG 1169

Qy       1065 TGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCA 1124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 TGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCA 1229

Qy       1125 GTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGT 1184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1230 GTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGT 1289

Qy       1185 GGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTT 1244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1290 GGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTT 1349

Qy       1245 TCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGT 1304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1350 TCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGT 1409

Qy       1305 CCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGA 1364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1410 CCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGA 1469

Qy       1365 TGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACAT 1424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1470 CGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACAT 1529
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Qy       1425 GAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCT 1484
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1530 GAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCT 1589

Qy       1485 CCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCT 1544
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1590 CCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCT 1649

Qy       1545 CTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCA 1604
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 CTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCA 1709

Qy       1605 TATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAG 1664
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1710 TATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAG 1769

Qy       1665 GCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCA 1724
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1770 GCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCA 1829

Qy       1725 CTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGC 1784
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1830 CTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGC 1889

Qy       1785 CTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTT 1844
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1890 CTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTT 1949

Qy       1845 CCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCT 1904
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1950 CCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCT 2009

Qy       1905 CCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGA 1964
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2010 CCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGA 2069

Qy       1965 TGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGA 2024
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2070 TGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGA 2129

Qy       2025 GGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGA 2084
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2130 GGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGA 2189

Qy       2085 CCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCA 2144
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2190 CCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCA 2249

Qy       2145 TCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCA 2204
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2250 TCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCA 2309

Qy       2205 GCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCAC 2264
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2310 GCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCAC 2369

Qy       2265 CCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTT 2324
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2370 CCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTT 2429

Qy       2325 GTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTC 2384
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2430 GTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTC 2489

Qy       2385 CCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGAC 2444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2490 CCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGAC 2549

Qy       2445 AGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAA 2504
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2550 AGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAA 2609

Qy       2505 GCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCT 2564
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2610 GCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCT 2669

Qy       2565 CGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGG 2624
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2670 CGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGG 2729

Qy       2625 TGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCT 2684
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2730 TGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCT 2789

Qy       2685 GAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAA 2744
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2790 GAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAA 2849

Qy       2745 CTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCT 2804
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2850 CTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCT 2909

Qy       2805 TCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTG 2864
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2910 TCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTG 2969

Qy       2865 TCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCT 2924
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2970 TCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCT 3029

Qy       2925 GAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGA 2984
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3030 GAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGA 3089

Qy       2985 GGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGAC 3044
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3090 GGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGAC 3149

Qy       3045 TTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCT 3104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3150 TTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCT 3209

Qy       3105 AAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGC 3164
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3210 AAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGC 3269

Qy       3165 CTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAAT 3224
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3270 CTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAAT 3329

Qy       3225 AAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTG 3284
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3330 AAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTG 3389

Qy       3285 GCATTCTTTTGATGAAGATGACCG 3308
             ||||||||||||||||||||||||
Db       3390 GCATTCTTTTGATGAAGATGACCG 3413
```

RESULT 6
AAL47135
ID AAL47135 standard; DNA; 5859 BP.
XX
AC AAL47135;
XX
DT 20-AUG-2002 (first entry)
XX
DE Pyrin domain containing protein NALP8/Py12 coding sequence.
XX
KW Pyrin domain; PYD domain; antiinflammatory; antiparkinsonian;
KW antiarteriosclerotic; antipsoriatic; antibacterial; virucide;
KW neuroprotective; antiarthritic; antirheumatic; antiasthmatic;
KW nephrotropic; osteopathic; nootropic; intracellular signal transduction;
KW inflammation; Alzheimer's disease; infection; psoriasis; asthma;
KW arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis;
KW osteoarthritis; glomerulonephritis; gene; ds.

XX
OS Unidentified.
XX
PN WO200240668-A2.
XX
PD 23-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-EP012545.
XX
PR 15-NOV-2000; 2000DE-01056687.
PR 30-NOV-2000; 2000DE-01059595.
XX
PA (APOT-) APOTECH RES & DEV LTD.
XX
PI Tschopp J, Martinon F;
XX
DR WPI; 2002-427093/45.
DR P-PSDB; AAO17863.
XX
PT New DNA encoding protein with pyrin domain, useful for treating diseases
PT involving impaired signal transduction, particularly inflammation, also
PT proteins and antibodies.
XX
PS Claim 5; Fig 1; 116pp; German.
XX
CC The present invention relates the DNA and their encoded proteins, where
CC the proteins contain at least one PYD (pyrin) domain. These can be used
CC to treat diseases associated with impaired intracellular signal
CC transduction, particularly inflammation such as psoriasis,
CC arteriosclerosis, bacterial or viral infections (particularly meningitis
CC and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma,
CC sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's
CC and Parkinson's diseases. The present sequence is a coding sequence of
CC the invention
XX
SQ Sequence 5859 BP; 1512 A; 1443 C; 1530 G; 1374 T; 0 U; 0 Other;

Query Match 69.5%; Score 2803; DB 6; Length 5859;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2903; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       290 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 349
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2387 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 2446

Qy       350 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 409
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2447 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 2506

Qy       410 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 469
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2507 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 2566

Qy       470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2567 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 2626

Qy       530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2627 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 2686

Qy       590 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 649
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2687 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 2746

Qy       650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2747 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 2806

Qy       710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2807 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 2866

Qy       770 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 829
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2867 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 2926

Qy       830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2927 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 2986

Qy       890 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 949
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2987 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 3046

Qy       950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3047 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 3106

Qy      1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3107 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 3166

Qy      1070 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 1129
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3167 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 3226

Qy      1130 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3227 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 3286

Qy      1190 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1249
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3287 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 3346

Qy      1250 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1309
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3347 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 3406

Qy      1310 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1369
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      3407 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTG 3466

Qy      1370 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3467 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 3526

Qy      1430 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1489
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3527 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 3586

Qy      1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3587 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 3646

Qy      1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3647 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 3706

Qy      1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3707 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 3766

Qy      1670 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1729
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3767 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 3826

Qy      1730 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 1789
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3827 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 3886

Qy      1790 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 1849
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3887 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 3946

Qy      1850 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 1909
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Db       3947 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 4006

Qy       1910 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 1969

Db       4007 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 4066

Qy       1970 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2029

Db       4067 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 4126

Qy       2030 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2089

Db       4127 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 4186

Qy       2090 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2149

Db       4187 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 4246

Qy       2150 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2209

Db       4247 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 4306

Qy       2210 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2269

Db       4307 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 4366

Qy       2270 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2329

Db       4367 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 4426

Qy       2330 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2389

Db       4427 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 4486

Qy       2390 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2449

Db       4487 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 4546

Qy       2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509

Db       4547 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 4606

Qy       2510 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2569

Db       4607 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 4666

Qy       2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629

Db       4667 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 4726

Qy       2630 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2689

Db       4727 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 4786

Qy       2690 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 2749

Db       4787 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 4846

Qy       2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809

Db       4847 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 4906

Qy       2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869

Db       4907 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 4966

Qy       2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929

Db       4967 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 5026

Qy       2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989

Db       5027 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGAC 5086

Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049

Db       5087 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 5146

Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109

Db       5147 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 5206

Qy       3110 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3169

Db       5207 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 5266

Qy       3170 CCACGTCTAACTTACAGATAATTGG 3194

Db       5267 CCACGTCTAACTTACAGATAATTGG 5291
```

RESULT 7
AAL47131
ID AAL47131 standard; DNA; 6939 BP.
XX
AC AAL47131;
XX
DT 20-AUG-2002 (first entry)
XX
DE Pyrin domain containing protein NALP5/Py8-hs coding sequence.
XX
KW Pyrin domain; PYD domain; antiinflammatory; antiparkinsonian;
KW antiarteriosclerotic; antipsoriatic; antibacterial; virucide;
KW neuroprotective; antiarthritic; antirheumatic; antiasthmatic;
KW nephrotropic; osteopathic; nootropic; intracellular signal transduction;
KW inflammation; Alzheimer's disease; infection; psoriasis; asthma;
KW arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis;
KW osteoarthritis; glomerulonephritis; gene; ds.
XX
OS Unidentified.
XX
PN WO200240668-A2.
XX
PD 23-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-EP012545.
XX
PR 15-NOV-2000; 2000DE-01056687.
PR 30-NOV-2000; 2000DE-01059595.
XX
PA (APOT-) APOTECH RES & DEV LTD.
XX
PI Tschopp J, Martinon F;
XX
DR WPI; 2002-427093/45.
DR P-PSDB; AAO17859.
XX
PT New DNA encoding protein with pyrin domain, useful for treating diseases
PT involving impaired signal transduction, particularly inflammation, also
PT proteins and antibodies.
XX
PS Claim 5; Fig 1; 116pp; German.
XX
CC The present invention relates the DNA and their encoded proteins, where
CC the proteins contain at least one PYD (pyrin) domain. These can be used
CC to treat diseases associated with impaired intracellular signal
CC transduction, particularly inflammation such as psoriasis,
CC arteriosclerosis, bacterial or viral infections (particularly meningitis
CC and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma,
CC sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's
CC and Parkinson's diseases. The present sequence is a coding sequence of
CC the invention
XX
SQ Sequence 6939 BP; 1791 A; 1719 C; 1801 G; 1628 T; 0 U; 0 Other;

```
Query Match             69.5%;  Score 2803;  DB 6;  Length 6939;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 2903;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        290 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 3526

Qy        350 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 3586

Qy        410 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 3646

Qy        470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 3706

Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 3766

Qy        590 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 3826

Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 3886

Qy        710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 3946

Qy        770 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3947 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 4006

Qy        830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4007 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 4066

Qy        890 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4067 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 4126

Qy        950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4127 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 4186

Qy       1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4187 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 4246

Qy       1070 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4247 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 4306

Qy       1130 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4307 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 4366

Qy       1190 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1249
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4367 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 4426

Qy       1250 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4427 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 4486

Qy       1310 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4487 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTG 4546

Qy       1370 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4547 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 4606

Qy       1430 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4607 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 4666

Qy       1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4667 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 4726

Qy       1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4727 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 4786

Qy       1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4787 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 4846

Qy       1670 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4847 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 4906

Qy       1730 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 1789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4907 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 4966

Qy       1790 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 1849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4967 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 5026

Qy       1850 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 1909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5027 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 5086

Qy       1910 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 1969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5087 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 5146

Qy       1970 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5147 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 5206

Qy       2030 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5207 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 5266

Qy       2090 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5267 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 5326

Qy       2150 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5327 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 5386

Qy       2210 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5387 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 5446

Qy       2270 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5447 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 5506

Qy       2330 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5507 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 5566

Qy       2390 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       5567 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 5626

Qy       2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5627 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 5686

Qy       2510 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5687 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 5746

Qy       2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5747 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 5806

Qy       2630 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5807 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 5866

Qy       2690 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 2749
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5867 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 5926

Qy       2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5927 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 5986

Qy       2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5987 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 6046

Qy       2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6047 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 6106

Qy       2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       6107 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGAC 6166

Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6167 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 6226

Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6227 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 6286

Qy       3110 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6287 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 6346

Qy       3170 CCACGTCTAACTTACAGATAATTGG 3194
             |||||||||||||||||||||||||
Db       6347 CCACGTCTAACTTACAGATAATTGG 6371


RESULT 8
AAL47140
ID   AAL47140 standard; DNA; 6939 BP.
XX
AC   AAL47140;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Pyrin domain containing protein NALP13/Py17 coding sequence.
XX
KW   Pyrin domain; PYD domain; antiinflammatory; antiparkinsonian;
KW   antiarteriosclerotic; antipsoriatic; antibacterial; virucide;
KW   neuroprotective; antiarthritic; antirheumatic; antiasthmatic;
KW   nephrotropic; osteopathic; nootropic; intracellular signal transduction;
KW   inflammation; Alzheimer's disease; infection; psoriasis; asthma;
KW   arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis;
KW   osteoarthritis; glomerulonephritis; gene; ds.
XX
OS   Unidentified.
XX
PN   WO200240668-A2.
XX
PD   23-MAY-2002.
XX
PF   30-OCT-2001; 2001WO-EP012545.
XX
PR   15-NOV-2000; 2000DE-01056687.
PR   30-NOV-2000; 2000DE-01059595.
XX
PA   (APOT-) APOTECH RES & DEV LTD.
XX
PI   Tschopp J,  Martinon F;
XX
DR   WPI; 2002-427093/45.
DR   P-PSDB; AAO17868.
XX
PT   New DNA encoding protein with pyrin domain, useful for treating diseases
PT   involving impaired signal transduction, particularly inflammation, also
PT   proteins and antibodies.
XX
PS   Claim 5; Fig 1; 116pp; German.
XX
CC   The present invention relates the DNA and their encoded proteins, where
CC   the proteins contain at least one PYD (pyrin) domain. These can be used
CC   to treat diseases associated with impaired intracellular signal
CC   transduction, particularly inflammation such as psoriasis,
CC   arteriosclerosis, bacterial or viral infections (particularly meningitis
CC   and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma,
CC   sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's
CC   and Parkinson's diseases. The present sequence is a coding sequence of
CC   the invention
XX
SQ   Sequence 6939 BP; 1791 A; 1719 C; 1801 G; 1628 T; 0 U; 0 Other;

  Query Match           69.5%;  Score 2803;  DB 6;  Length 6939;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2903;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        290 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 3526

Qy        350 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3527 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 3586

Qy        410 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 3646

Qy        470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3647 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 3706

Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3707 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 3766

Qy        590 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3767 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 3826

Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3827 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 3886

Qy        710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3887 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 3946

Qy        770 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 829
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Db      3947 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 4006
Qy       830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
Db      4007 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 4066
Qy       890 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 949
Db      4067 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 4126
Qy       950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
Db      4127 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 4186
Qy      1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
Db      4187 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 4246
Qy      1070 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 1129
Db      4247 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 4306
Qy      1130 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1189
Db      4307 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 4366
Qy      1190 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1249
Db      4367 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 4426
Qy      1250 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1309
Db      4427 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 4486
Qy      1310 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1369
Db      4487 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTG 4546
Qy      1370 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1429
Db      4547 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 4606
Qy      1430 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1489
Db      4607 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 4666
Qy      1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
Db      4667 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 4726
Qy      1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
Db      4727 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 4786
Qy      1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
Db      4787 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 4846
Qy      1670 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1729
Db      4847 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 4906
Qy      1730 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 1789
Db      4907 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 4966
Qy      1790 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 1849
Db      4967 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 5026
Qy      1850 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 1909
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Db      5027 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 5086
Qy      1910 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 1969
Db      5087 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 5146
Qy      1970 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2029
Db      5147 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 5206
Qy      2030 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2089
Db      5207 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 5266
Qy      2090 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2149
Db      5267 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 5326
Qy      2150 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2209
Db      5327 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 5386
Qy      2210 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2269
Db      5387 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 5446
Qy      2270 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2329
Db      5447 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 5506
Qy      2330 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2389
Db      5507 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 5566
Qy      2390 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2449
Db      5567 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 5626
Qy      2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509
Db      5627 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 5686
Qy      2510 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2569
Db      5687 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 5746
Qy      2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629
Db      5747 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 5806
Qy      2630 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2689
Db      5807 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 5866
Qy      2690 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 2749
Db      5867 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 5926
Qy      2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809
Db      5927 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 5986
Qy      2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869
Db      5987 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 6046
Qy      2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929
Db      6047 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 6106
Qy      2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989
Db      6107 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGAC 6166
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Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
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Db       6167 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 6226

Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
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Db       6227 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 6286

Qy       3110 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6287 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 6346

Qy       3170 CCACGTCTAACTTACAGATAATTGG 3194
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Db       6347 CCACGTCTAACTTACAGATAATTGG 6371
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RESULT 9
ABX97181
ID   ABX97181 standard; cDNA; 3226 BP.
XX
AC   ABX97181;
XX
DT   20-MAY-2003  (first entry)
XX
DE   Human NOV125b cDNA.
XX
KW   NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;
KW   hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
KW   human; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200272757-A2.
XX
PD   19-SEP-2002.
XX
PF   08-MAR-2002; 2002WO-US006908.
XX
PR   08-MAR-2001; 2001US-0274101P.
PR   08-MAR-2001; 2001US-0274194P.
PR   08-MAR-2001; 2001US-0274281P.
PR   08-MAR-2001; 2001US-0274322P.
PR   09-MAR-2001; 2001US-0274849P.
PR   12-MAR-2001; 2001US-0275235P.
PR   13-MAR-2001; 2001US-0275578P.
PR   13-MAR-2001; 2001US-0275579P.
PR   13-MAR-2001; 2001US-0275601P.
PR   14-MAR-2001; 2001US-0276000P.
PR   16-MAR-2001; 2001US-0276776P.
PR   19-MAR-2001; 2001US-0276994P.
PR   20-MAR-2001; 2001US-0277239P.
PR   20-MAR-2001; 2001US-0277321P.
PR   20-MAR-2001; 2001US-0277327P.
PR   21-MAR-2001; 2001US-0277791P.
PR   22-MAR-2001; 2001US-0277833P.
PR   23-MAR-2001; 2001US-0278152P.
PR   26-MAR-2001; 2001US-0278894P.
PR   27-MAR-2001; 2001US-0278999P.
PR   27-MAR-2001; 2001US-0279036P.
PR   28-MAR-2001; 2001US-0279344P.
PR   30-MAR-2001; 2001US-0277338P.
PR   30-MAR-2001; 2001US-0279995P.
PR   30-MAR-2001; 2001US-0280233P.
PR   02-APR-2001; 2001US-0280802P.
PR   02-APR-2001; 2001US-0280822P.
PR   02-APR-2001; 2001US-0280900P.
PR   04-APR-2001; 2001US-0281194P.
PR   13-APR-2001; 2001US-0283675P.
PR   30-APR-2001; 2001US-0287424P.
PR   02-MAY-2001; 2001US-0288066P.
PR   03-MAY-2001; 2001US-0288342P.
PR   03-MAY-2001; 2001US-0288528P.
PR   15-MAY-2001; 2001US-0291190P.
PR   16-MAY-2001; 2001US-0291099P.
PR   16-MAY-2001; 2001US-0291240P.
PR   30-MAY-2001; 2001US-0294485P.
PR   31-MAY-2001; 2001US-0294889P.
PR   31-MAY-2001; 2001US-0294899P.
PR   18-JUN-2001; 2001US-0299027P.
PR   19-JUN-2001; 2001US-0299303P.
PR   19-JUN-2001; 2001US-0299310P.
PR   10-JUL-2001; 2001US-0304354P.
PR   31-JUL-2001; 2001US-0309198P.
PR   16-AUG-2001; 2001US-0312903P.
PR   10-SEP-2001; 2001US-0318462P.
PR   12-SEP-2001; 2001US-0318770P.
PR   27-SEP-2001; 2001US-0325430P.
PR   27-SEP-2001; 2001US-0325681P.
PR   18-OCT-2001; 2001US-0330380P.
PR   31-OCT-2001; 2001US-0335301P.
PR   14-NOV-2001; 2001US-0332172P.
PR   14-NOV-2001; 2001US-0332271P.
PR   14-NOV-2001; 2001US-0332272P.
PR   14-NOV-2001; 2001US-0333184P.
PR   14-NOV-2001; 2001US-0333272P.
PR   21-NOV-2001; 2001US-0332094P.
PR   03-DEC-2001; 2001US-0337426P.
PR   03-DEC-2001; 2001US-0338092P.
PR   04-DEC-2001; 2001US-0337185P.
PR   03-JAN-2002; 2002US-0345705P.
PR   07-MAR-2002; 2002US-00092900.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Padigaru M,  Spytek KA,  Shenoy SG,  Taupier RJ,  Pena CEA,  Li L;
PI   Zerhusen BD,  Gusev V,  Ji W,  Gorman L,  Miller CE,  Kekuda R;
PI   Patturajan M,  Gangolli E,  Vernet CAM,  Guo X,  Tchernev V;
PI   Fernandes ER,  Casman SJ,  Malyankar UM,  Gerlach V,  Liu Y,  Anderson D;
PI   Spaderna SK,  Catterton E,  Burgess C,  Leite M,  Zhong H,  Alsobrook JP;
PI   Lepley DM,  Rieger DK;
XX
DR   WPI; 2002-723332/78.
DR   P-PSDB; ABU65214.
XX
PT   NOVX polypeptides and polynucleotides, useful for preventing or treating
PT   a disorder associated with aberrant NOVX expression or activity e.g.,
PT   cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
PT   asthma.
XX
PS   Claim 13; Page 467; 1103pp; English.
XX
CC   This invention describes novel human NOVX polypeptides which have
CC   cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive
CC   activity. Pharmaceutical compositions comprising the NOVX proteins or
CC   nucleic acid molecules or NOVX antibodies are useful for preventing or
CC   treating a disorder associated with aberrant NOVX expression or activity
CC   e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC   asthma. The products of the invention can be used for gene therapy or in
CC   a vaccine. ABX97008-ABX97185 are cDNA fragments amplified and isolated by
CC   the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-
CC   ABX97593. ABX97008-ABX97185 encode the NOVX proteins described in
CC   ABU65041-ABU65218
XX
SQ   Sequence 3226 BP; 738 A; 856 C; 914 G; 718 T; 0 U; 0 Other;

  Query Match           69.4%;  Score 2801;  DB 6;  Length 3226;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2901;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        406 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 308

Qy        466 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 525
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Db        309 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 368
Qy        526 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 585
Db        369 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 428
Qy        586 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 645
Db        429 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 488
Qy        646 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 705
Db        489 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 548
Qy        706 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 765
Db        549 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 608
Qy        766 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 825
Db        609 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 668
Qy        826 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 885
Db        669 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 728
Qy        886 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 945
Db        729 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 788
Qy        946 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 1005
Db        789 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 848
Qy       1006 TTAGTTAGAGGAATCTCCGGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 1065
Db        849 TTAGTTAGAGGAATCTCCGGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 908
Qy       1066 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 1125
Db        909 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 968
Qy       1126 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1185
Db        969 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1028
Qy       1186 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1245
Db       1029 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1088
Qy       1246 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1305
Db       1089 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1148
Qy       1306 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAT 1365
Db       1149 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAC 1208
Qy       1366 GGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATG 1425
Db       1209 GGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATG 1268
Qy       1426 AACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTC 1485
Db       1269 AACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTC 1328
Qy       1486 CAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTC 1545
Db       1329 CAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTC 1388
Qy       1546 TGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCAT 1605
Db       1389 TGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCAT 1448
Qy       1606 ATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGG 1665
Db       1449 ATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGG 1508
Qy       1666 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1725
Db       1509 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1568
Qy       1726 TGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCC 1785
Db       1569 TGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCC 1628
Qy       1786 TTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTC 1845
Db       1629 TTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTC 1688
Qy       1846 CAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTC 1905
Db       1689 CAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTC 1748
Qy       1906 CAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGAT 1965
Db       1749 CAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGAT 1808
Qy       1966 GAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAG 2025
Db       1809 GAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAG 1868
Qy       2026 GAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGAC 2085
Db       1869 GAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGAC 1928
Qy       2086 CTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCAT 2145
Db       1929 CTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCAT 1988
Qy       2146 CCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAG 2205
Db       1989 CCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAG 2048
Qy       2206 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2265
Db       2049 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2108
Qy       2266 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2325
Db       2109 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2168
Qy       2326 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2385
Db       2169 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2228
Qy       2386 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2445
Db       2229 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2288
Qy       2446 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAG 2505
Db       2289 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAG 2348
Qy       2506 CTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTC 2565
Db       2349 CTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTC 2408
Qy       2566 GTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGT 2625
Db       2409 GTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGT 2468
Qy       2626 GTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTG 2685
Db       2469 GTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTG 2528
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Qy       2686 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2745
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Db       2529 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2588

Qy       2746 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2805
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Db       2589 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2648

Qy       2806 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2865
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Db       2649 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2708

Qy       2866 CATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTG 2925
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Db       2709 CATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTG 2768

Qy       2926 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAG 2985
             ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       2769 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAG 2828

Qy       2986 GGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACT 3045
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2829 GGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACT 2888

Qy       3046 TCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTA 3105
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Db       2889 TCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTA 2948

Qy       3106 AACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCC 3165
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Db       2949 AACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCC 3008

Qy       3166 TGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATA 3225
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Db       3009 TGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATA 3068

Qy       3226 AGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGG 3285
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3069 AGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGG 3128

Qy       3286 CATTCTTTTGATGAAGATGACCG 3308
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Db       3129 CATTCTTTTGATGAAGATGACCG 3151
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RESULT 10
ABK48628
ID   ABK48628 standard; cDNA; 3900 BP.
XX
AC   ABK48628;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Human MATER cDNA.
XX
KW   Human; gene; ss; contraceptive; antiinfertility; MATER;
KW   maternal antigen that embryos require; MATER null phenotype; oocyte;
KW   early embryonic survival; premature ovarian failure; POF;
KW   autoimmune infertility; chromosome 19; gene therapy; fertility.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3603
FT                   /*tag=  a
FT                   /product= "Human MATER"
XX
PN   WO200232955-A1.
XX
PD   25-APR-2002.
XX
PF   04-APR-2001; 2001WO-US010981.
XX
PR   18-OCT-2000; 2000US-0241510P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nelson LM,  Tong Z;
XX
DR   WPI; 2002-454595/48.
DR   P-PSDB; AAU79526.
XX
PT   New isolated human Maternal Antigen That Embryos Require protein and
PT   polynucleotide, useful in diagnosing or treating fertility or reduced
PT   fertility, or as a contraceptive.
XX
PS   Claim 11; Page 80-85; 93pp; English.
XX
CC   The invention discloses an isolated human MATER (Maternal Antigen That
CC   Embryos Require) protein, which can complement a MATER null phenotype in
CC   which zygotes arising from the oocyte do not progress beyond the two-cell
CC   stage. MATER is required for early embryonic survival and abnormal levels
CC   of the protein can lead to premature ovarian failure (POF) and can be
CC   caused by under or over expression of MATER or an autoimmune response to
CC   MATER. MATER is a single-copy maternal effect gene found on chromosome
CC   19. The MATER protein and polynucleotide, by gene therapy, are useful in
CC   diagnosing or treating fertility and reduced fertility. In particular,
CC   the MATER protein is useful as a contraceptive agent, or for influencing
CC   (either inhibiting or enhancing) fertility and can be used to detect a
CC   predisposition to infertility or reduced fertility, or for presymptomatic
CC   screening of an individual for infertility/reduced fertility. The protein
CC   and polynucleotide are also useful for detecting an excess or deficiency,
CC   or genetic mutation, of the MATER protein in a mammalian subject (e.g. a
CC   human or a mouse) or for screening for a compound useful in influencing
CC   MATER-mediated fertility. The sequence presented is the human MATER cDNA.
CC   Note: Nucleotides 1-75 were deduced, by the inventors, by comparison to
CC   published human genomic DNA sequences, while the remainder of the
CC   sequence was determined by direct cloning of human ovarian cDNAs
XX
SQ   Sequence 3900 BP; 981 A; 987 C; 1044 G; 888 T; 0 U; 0 Other;
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  Query Match             67.2%;  Score 2713;  DB 6;  Length 3900;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 3013;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        290 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 625

Qy        350 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 685

Qy        410 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 745

Qy        470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 805

Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        806 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 865

Qy        590 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 925

Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        926 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 985

Qy        710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        986 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 1045
Qy        770 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1046 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 1105
Qy        830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1106 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 1165
Qy        890 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1166 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 1225
Qy        950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1226 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1285
Qy       1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1286 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1345
Qy       1070 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 1129
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1346 ATCAGAAGACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCC 1405
Qy       1130 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1406 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1465
Qy       1190 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1249
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db       1466 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATC 1525
Qy       1250 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1309
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1526 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1585
Qy       1310 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1369
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1586 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1645
Qy       1370 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1429
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1646 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1705
Qy       1430 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1489
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1706 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1765
Qy       1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1766 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1825
Qy       1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1826 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1885
Qy       1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1886 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1945
Qy       1670 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1729
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1946 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 2005
Qy       1730 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 1789
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2006 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 2065
Qy       1790 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 1849
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2066 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 2125

Qy       1850 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 1909
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2126 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 2185
Qy       1910 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 1969
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2186 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 2245
Qy       1970 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2029
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2246 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2305
Qy       2030 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2306 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2365
Qy       2090 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2366 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2425
Qy       2150 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2209
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       2426 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACC 2485
Qy       2210 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2486 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2545
Qy       2270 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2546 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2605
Qy       2330 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2389
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2606 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2665
Qy       2390 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2449
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2666 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2725
Qy       2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2726 AGGGAGTAACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2785
Qy       2510 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2569
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2786 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2845
Qy       2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2846 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2905
Qy       2630 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2689
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2906 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2965
Qy       2690 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 2749
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       2966 AGTGCCACCTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCAT 3025
Qy       2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3026 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 3085
Qy       2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3086 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 3145
Qy       2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3146 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 3205
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Qy       2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3206 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 3265

Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3266 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3325

Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3326 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3385

Qy       3110 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3386 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3445

Qy       3170 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3446 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3505

Qy       3230 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3506 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3565

Qy       3290 CTTTTGATGAAGATGACCG 3308
             |||||||||||||||||||
Db       3566 CTTTTGATGAAGATGACCG 3584
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RESULT 11
AAD49018
ID AAD49018 standard; cDNA; 3900 BP.
XX
AC AAD49018;
XX
DT 07-MAR-2003 (first entry)
XX
DE Human MATER cDNA.
XX
KW Human; MATER protein; infertility; fertility; contraceptive agent;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .3603
FT /*tag= a
FT /product= "Human MATER protein"
XX
PN WO200281492-A1.
XX
PD 17-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009776.
XX
PR 04-APR-2001; 2001WO-US010981.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nelson LM, Tong Z;
XX
DR WPI; 2003-058494/05.
DR P-PSDB; AAE31749.
XX
PT New isolated variant MATER proteins and nucleic acids, useful for
PT diagnosing, prognosing and treating infertility and reduced fertility,
PT and as contraceptive agents.
XX
PS Example 2; Page 93-98; 110pp; English.
XX
CC The present invention relates to novel MATER proteins and polynucleotides
CC encoding such proteins. The MATER proteins are essential to fertility.
CC Sequences of the invention are useful for diagnosing, prognosing and
CC treating infertility, reduced fertility and as contraceptive agents. They
CC are also useful in gene therapy. The method is useful for detecting a
CC predisposition to or pre-symptomatic screening of an individual for
CC infertility or reduced fertility. The present sequence is human MATER
CC cDNA
XX
SQ Sequence 3900 BP; 981 A; 987 C; 1044 G; 888 T; 0 U; 0 Other;

Query Match 67.2%; Score 2713; DB 8; Length 3900;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3013; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        290 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 625

Qy        350 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 685

Qy        410 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 745

Qy        470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 805

Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        806 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 865

Qy        590 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 925

Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        926 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 985

Qy        710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        986 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 1045

Qy        770 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 829
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1046 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 1105

Qy        830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1106 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 1165

Qy        890 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1166 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 1225

Qy        950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1226 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1285

Qy       1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1286 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1345

Qy       1070 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 1129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1346 ATCAGAAGACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCC 1405

Qy       1130 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1189
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1406 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1465

Qy       1190 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1249
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Db      1466 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATC 1525

Qy      1250 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1526 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1585

Qy      1310 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1586 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1645

Qy      1370 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1646 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1705

Qy      1430 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1706 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1765

Qy      1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1766 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1825

Qy      1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1826 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1885

Qy      1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1886 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1945

Qy      1670 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1729
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1946 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 2005

Qy      1730 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 1789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2006 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 2065

Qy      1790 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 1849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2066 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 2125

Qy      1850 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 1909
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2126 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 2185

Qy      1910 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 1969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2186 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 2245

Qy      1970 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2246 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2305

Qy      2030 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2306 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2365

Qy      2090 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2366 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2425

Qy      2150 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      2426 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACC 2485

Qy      2210 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2486 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2545

Qy      2270 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2329
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db      2546 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2605

Qy      2330 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2606 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2665

Qy      2390 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2666 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2725

Qy      2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509
             |||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||
Db      2726 AGGGAGTAACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2785

Qy      2510 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2786 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2845

Qy      2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2846 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2905

Qy      2630 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2906 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2965

Qy      2690 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 2749
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db      2966 AGTGCCACCTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCAT 3025

Qy      2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3026 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 3085

Qy      2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3086 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 3145

Qy      2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3146 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 3205

Qy      2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3206 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 3265

Qy      2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3266 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3325

Qy      3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3326 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3385

Qy      3110 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3386 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3445

Qy      3170 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3446 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3505

Qy      3230 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3506 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3565

Qy      3290 CTTTTGATGAAGATGACCG 3308
             ||||||||||||||||||
Db      3566 CTTTTGATGAAGATGACCG 3584


RESULT 12
ABK48609
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ID   ABK48609 standard; cDNA; 1157 BP.
XX
AC   ABK48609;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Human MATER cDNA fragment #1.
XX
KW   Human; gene; ss; contraceptive; antiinfertility; MATER;
KW   Maternal antigen that embryos require; MATER null phenotype; oocyte;
KW   early embryonic survival; premature ovarian failure; POF;
KW   autoimmune infertility; chromosome 19; gene therapy; fertility.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1155
FT                   /*tag=  a
FT                   /product= "Human MATER"
FT                   /partial
FT                   /note= "No start or stop codon shown"
XX
PN   WO200232955-A1.
XX
PD   25-APR-2002.
XX
PF   04-APR-2001; 2001WO-US010981.
XX
PR   18-OCT-2000; 2000US-0241510P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nelson LM,  Tong Z;
XX
DR   WPI; 2002-454595/48.
DR   P-PSDB; AAU79523.
XX
PT   New isolated human Maternal Antigen That Embryos Require protein and
PT   polynucleotide, useful in diagnosing or treating fertility or reduced
PT   fertility, or as a contraceptive.
XX
PS   Claim 11; Page 68-69; 93pp; English.
XX
CC   The invention discloses an isolated human MATER (Maternal Antigen That
CC   Embryos Require) protein, which can complement a MATER null phenotype in
CC   which zygotes arising from the oocyte do not progress beyond the two-cell
CC   stage. MATER is required for early embryonic survival and abnormal levels
CC   of the protein can lead to premature ovarian failure (POF) and can be
CC   caused by under or over expression of MATER or an autoimmune response to
CC   MATER. MATER is a single-copy Maternal effect gene found on chromosome
CC   19. The MATER protein and polynucleotide, by gene therapy, are useful in
CC   diagnosing or treating fertility and reduced fertility. In particular,
CC   the MATER protein is useful as a contraceptive agent, or for influencing
CC   (either inhibiting or enhancing) fertility and can be used to detect a
CC   predisposition to infertility or reduced fertility, or for presymptomatic
CC   screening of an individual for infertility/reduced fertility. The protein
CC   and polynucleotide are also useful for detecting an excess or deficiency,
CC   or genetic mutation, of the MATER protein in a mammalian subject (e.g. a
CC   human or a mouse) or for screening for a compound useful in influencing
CC   MATER-mediated fertility. The sequence presented is the human MATER cDNA
CC   fragment #1, which was isolated from a human cDNA library
XX
SQ   Sequence 1157 BP; 240 A; 324 C; 320 G; 273 T; 0 U; 0 Other;

  Query Match            27.3%;  Score 1102;  DB 6;  Length 1157;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 1152;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        757 GCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTC 816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTC 63

Qy        817 GATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 123

Qy        877 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 183

Qy        937 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 996
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 243

Qy        997 CGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGC 1056
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGC 303

Qy       1057 GGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTG 1116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTG 363

Qy       1117 CTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAG 1176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAG 423

Qy       1177 GACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCT 1236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCT 483

Qy       1237 TTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAA 1296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAA 543

Qy       1297 AGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCA 1356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCA 603

Qy       1357 GTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTG 1416
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 GTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTG 663

Qy       1417 TTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCAC 1476
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 TTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCAC 723

Qy       1477 CTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAG 1536
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 CTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAG 783

Qy       1537 CCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCA 1596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 CCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCA 843

Qy       1597 GGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGAC 1656
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGAC 903

Qy       1657 GTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAG 1716
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 GTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAG 963

Qy       1717 CTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACC 1776
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 CTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACC 1023

Qy       1777 CTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTA 1836
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 CTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTA 1083

Qy       1837 AACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCC 1896
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 AACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCC 1143

Qy       1897 TTCTGCCTCCAGC 1909
              |||||||||||||
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Db       1144 TTCTGCCTCCAGC 1156


RESULT 13
AAD48999
ID   AAD48999 standard; cDNA; 1157 BP.
XX
AC   AAD48999;
XX
DT   07-MAR-2003  (first entry)
XX
DE   Human MATER cDNA fragment 1.
XX
KW   Human; MATER protein; infertility; fertility; contraceptive agent;
KW   gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1155
FT                   /*tag= a
FT                   /product= "Human MATER protein fragment 1"
FT                   /transl_except= (pos:112. .114, aa:Thr)
FT                   /transl_except= (pos:589. .591, aa:Thr)
FT                   /transl_except= (pos:865. .867, aa:Thr)
FT                   /transl_except= (pos:973. .975, aa:Thr)
FT                   /transl_except= (pos:1102. .1104, aa:Thr)
FT                   /note= "No start and stop codon"
FT                   /partial
XX
PN   WO200281492-A1.
XX
PD   17-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-US009776.
XX
PR   04-APR-2001; 2001WO-US010981.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nelson LM,  Tong Z;
XX
DR   WPI; 2003-058494/05.
DR   P-PSDB; AAE31746.
XX
PT   New isolated variant MATER proteins and nucleic acids, useful for
PT   diagnosing, prognosing and treating infertility and reduced fertility,
PT   and as contraceptive agents.
XX
PS   Example 2; Page 79-80; 110pp; English.
XX
CC   The present invention relates to novel MATER proteins and polynucleotides
CC   encoding such proteins. The MATER proteins are essential to fertility.
CC   Sequences of the invention are useful for diagnosing, prognosing and
CC   treating infertility, reduced fertility and as contraceptive agents. They
CC   are also useful in gene therapy. The method is useful for detecting a
CC   predisposition to or pre-symptomatic screening of an individual for
CC   infertility or reduced fertility. The present sequence is human MATER
CC   cDNA fragment 1
XX
SQ   Sequence 1157 BP; 240 A; 324 C; 320 G; 273 T; 0 U; 0 Other;

  Query Match             27.3%;  Score 1102;  DB 8;  Length 1157;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1152;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        757 GCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTC 816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTC 63

Qy        817 GATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 123

Qy        877 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 183

Qy        937 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 996
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 243

Qy        997 CGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGC 1056
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGC 303

Qy       1057 GGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTG 1116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTG 363

Qy       1117 CTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAG 1176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAG 423

Qy       1177 GACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCT 1236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCT 483

Qy       1237 TTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAA 1296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAA 543

Qy       1297 AGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCA 1356
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Db        544 AGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCA 603

Qy       1357 GTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTG 1416
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 GTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTG 663

Qy       1417 TTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCAC 1476
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 TTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCAC 723

Qy       1477 CTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAG 1536
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 CTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAG 783

Qy       1537 CCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCA 1596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 CCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCA 843

Qy       1597 GGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGAC 1656
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGAC 903

Qy       1657 GTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAG 1716
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Db        904 GTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAG 963

Qy       1717 CTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACC 1776
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 CTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACC 1023

Qy       1777 CTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTA 1836
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Db       1024 CTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTA 1083

Qy       1837 AACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCC 1896
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Db       1084 AACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCC 1143

Qy       1897 TTCTGCCTCCAGC 1909
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Db       1144 TTCTGCCTCCAGC 1156
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RESULT 14
ABK48610
ID   ABK48610 standard; cDNA; 1075 BP.
XX
AC   ABK48610;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Human MATER cDNA fragment #2.
XX
KW   Human; gene; ss; contraceptive; antiinfertility; MATER;
KW   maternal antigen that embryos require; MATER null phenotype; oocyte;
KW   early embryonic survival; premature ovarian failure; POF;
KW   autoimmune infertility; chromosome 19; gene therapy; fertility.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             2. .778
FT                   /*tag= a
FT                   /product= "Human MATER"
FT                   /partial
FT                   /note= "No start codon shown"
XX
PN   WO200232955-A1.
XX
PD   25-APR-2002.
XX
PF   04-APR-2001; 2001WO-US010981.
XX
PR   18-OCT-2000; 2000US-0241510P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nelson LM,  Tong Z;
XX
DR   WPI; 2002-454595/48.
DR   P-PSDB; AAU79524.
XX
PT   New isolated human Maternal Antigen That Embryos Require protein and
PT   polynucleotide, useful in diagnosing or treating fertility or reduced
PT   fertility, or as a contraceptive.
XX
PS   Claim 11; Page 70-71; 93pp; English.
XX
CC   The invention discloses an isolated human MATER (Maternal Antigen That
CC   Embryos Require) protein, which can complement a MATER null phenotype in
CC   which zygotes arising from the oocyte do not progress beyond the two-cell
CC   stage. MATER is required for early embryonic survival and abnormal levels
CC   of the protein can lead to premature ovarian failure (POF) and can be
CC   caused by under or over expression of MATER or an autoimmune response to
CC   MATER. MATER is a single-copy maternal effect gene found on chromosome
CC   19. The MATER protein and polynucleotide, by gene therapy, are useful in
CC   diagnosing or treating fertility and reduced fertility. In particular,
CC   the MATER protein is useful as a contraceptive agent, or for influencing
CC   (either inhibiting or enhancing) fertility and can be used to detect a
CC   predisposition to infertility or reduced fertility, or for presymptomatic
CC   screening of an individual for infertility/reduced fertility. The protein
CC   and polynucleotide are also useful for detecting an excess or deficiency,
CC   or genetic mutation, of the MATER protein in a mammalian subject (e.g. a
CC   human or a mouse) or for screening for a compound useful in influencing
CC   MATER-mediated fertility. The sequence presented is the human MATER cDNA
CC   fragment #2, which was isolated from a human cDNA library
XX
SQ   Sequence 1075 BP; 278 A; 251 C; 281 G; 265 T; 0 U; 0 Other;

  Query Match           16.3%;  Score 657;  DB 6;  Length 1075;
  Best Local Similarity   99.7%;  Pred. No. 1.7e-297;
  Matches  757;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2550 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 2609
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Db          1 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 60

Qy       2610 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 2669
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Db         61 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 120

Qy       2670 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACT 2729
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Db        121 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTCTCTTGCACT 180

Qy       2730 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 2789
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Db        181 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 240

Qy       2790 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 2849
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Db        241 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 300

Qy       2850 GGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 2909
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Db        301 GGAGTTGGTAAAATGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 360

Qy       2910 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 2969
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Db        361 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 420

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Db        421 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 480

Qy       3030 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 3089
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Db        481 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 540

Qy       3090 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 3149
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Db        541 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 600

Qy       3150 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 3209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        601 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 660

Qy       3210 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 3269
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Db        661 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 720

Qy       3270 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 3308
             |||||||||||||||||||||||||||||||||||||||
Db        721 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 759


RESULT 15
AAD49000
ID   AAD49000 standard; cDNA; 1075 BP.
XX
AC   AAD49000;
XX
DT   07-MAR-2003  (first entry)
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DE   Human MATER cDNA fragment 2.
XX
KW   Human; MATER protein; infertility; fertility; contraceptive agent;
KW   gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /transl_except= (pos:200. .202, aa:Thr)
FT                   /transl_except= (pos:650. .652, aa:Thr)
FT                   /transl_except= (pos:656. .658, aa:Thr)
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FT                   /transl_except= (pos:767. .769, aa:Thr)
FT                   /note= "No start codon"
FT                   /partial
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PN   WO200281492-A1.
XX
PD   17-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-US009776.
XX
PR   04-APR-2001; 2001WO-US010981.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nelson LM,  Tong Z;
XX
DR   WPI; 2003-058494/05.
DR   P-PSDB; AAE31747.
XX
PT   New isolated variant MATER proteins and nucleic acids, useful for
PT   diagnosing, prognosing and treating infertility and reduced fertility,
PT   and as contraceptive agents.
XX
PS   Example 2; Page 81-82; 110pp; English.
XX
CC   The present invention relates to novel MATER proteins and polynucleotides
CC   encoding such proteins. The MATER proteins are essential to fertility.
CC   Sequences of the invention are useful for diagnosing, prognosing and
CC   treating infertility, reduced fertility and as contraceptive agents. They
CC   are also useful in gene therapy. The method is useful for detecting a
CC   predisposition to or pre-symptomatic screening of an individual for
CC   infertility or reduced fertility. The present sequence is human MATER
CC   cDNA fragment 2
XX
SQ   Sequence 1075 BP; 278 A; 251 C; 281 G; 265 T; 0 U; 0 Other;

  Query Match           16.3%;  Score 657;  DB 8;  Length 1075;
  Best Local Similarity  99.7%;  Pred. No. 1.7e-297;
  Matches  757;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2550 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 2609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 60

Qy       2610 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 2669
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Qy       2670 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACT 2729
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Qy       2730 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 2789
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Qy       2790 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 2849
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Db        361 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 420

Qy       2970 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 3029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 480

Qy       3030 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 3089
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Db        481 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG. 540

Qy       3090 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 3149
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Db        541 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 600

Qy       3150 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 3209
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Db        601 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 660

Qy       3210 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 3269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 720

Qy       3270 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 3308
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Db        721 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 759

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Job time : 2018 secs
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GenCore version 5.1.6

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Gapop 60.0 , Gapext 60.0

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SUMMARIES

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c	1	20	0.5	601	4	US-09-949-016-91585	Sequence 91585, A
c	2	20	0.5	601	4	US-09-949-016-91586	Sequence 91586, A
c	3	20	0.5	6042	1	US-08-261-822A-1	Sequence 1, Appli
c	4	20	0.5	6042	5	PCT-US95-07744A-1	Sequence 1, Appli
c	5	20	0.5	6172	2	US-08-819-288-1	Sequence 1, Appli
c	6	20	0.5	6172	3	US-09-400-348-1	Sequence 1, Appli
	7	20	0.5	8733	4	US-10-144-198-11	Sequence 11, Appl
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	39	19	0.5	60417	4	US-09-949-016-13312	Sequence 13312, A
	40	19	0.5	71251	4	US-09-949-016-15332	Sequence 15332, A
	41	19	0.5	209210	4	US-09-949-016-15094	Sequence 15094, A
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	45	19	0.5	278866	4	US-09-949-016-13925	Sequence 13925, A

ALIGNMENTS

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; Sequence 91585, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91585
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-91585

Query Match 0.5%; Score 20; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2398 ACCTCCCCCAGCCTGAAATC 2417
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Db 476 ACCTCCCCCAGCCTGAAATC 457

RESULT 2
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; Sequence 91586, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91586
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;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-91586

  Query Match             0.5%;  Score 20;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 26;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2398 ACCTCCCCCAGCCTGAAATC 2417
              ||||||||||||||||||||
Db        290 ACCTCCCCCAGCCTGAAATC 271


RESULT 3
US-08-261-822A-1/c
; Sequence 1, Application US/08261822A
; Patent No. 5650553
;  GENERAL INFORMATION:
;    APPLICANT:  Ecker, Joseph R. et al.
;    TITLE OF INVENTION:  Plant Genes for Sensitivity to Ethylene
;    TITLE OF INVENTION:  and Pathogens
;    NUMBER OF SEQUENCES:  82
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/261,822A
;      FILING DATE:  17-JUN-1994
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Beardell, Lori Y.
;      REGISTRATION NUMBER:  34,293
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6042 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-261-822A-1

  Query Match             0.5%;  Score 20;  DB 1;  Length 6042;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        966 AGAGAAGCTCAAGTCAGAGG 985
              ||||||||||||||||||||
Db       2046 AGAGAAGCTCAAGTCAGAGG 2027


RESULT 4
PCT-US95-07744A-1/c
; Sequence 1, Application PC/TUS9507744A
;  GENERAL INFORMATION:
;    APPLICANT:  Trustees of The University of Pennsylvania
;    TITLE OF INVENTION:  Plant Genes for Sensitivity to Ethylene
;    TITLE OF INVENTION:  and Pathogens
;    NUMBER OF SEQUENCES:  82
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & Norris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/07744A
;      FILING DATE:  15-JUNE-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/261,822
;      FILING DATE:  June 17, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Beardell, Lori Y.
;      REGISTRATION NUMBER:  34,293
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6042 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
PCT-US95-07744A-1

  Query Match             0.5%;  Score 20;  DB 5;  Length 6042;
  Best Local Similarity   100.0%;  Pred. No. 30;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        966 AGAGAAGCTCAAGTCAGAGG 985
              ||||||||||||||||||||
Db       2046 AGAGAAGCTCAAGTCAGAGG 2027


RESULT 5
US-08-819-288-1/c
; Sequence 1, Application US/08819288
; Patent No. 5955652
;  GENERAL INFORMATION:
;    APPLICANT:  Ecker, Joseph
;    APPLICANT:  Alonso, Jose
;    TITLE OF INVENTION:  PLANT GENES FOR SENSITIVITY TO ETHYLENE
;    TITLE OF INVENTION:  AND PATHOGENS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5955652ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,288
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;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Beardell, Lori Y.
;      REGISTRATION NUMBER:  34,293
;      REFERENCE/DOCKET NUMBER:  UPN-2949
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6172 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-819-288-1

  Query Match             0.5%;  Score 20;  DB 2;  Length 6172;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        966 AGAGAAGCTCAAGTCAGAGG 985
              ||||||||||||||||||||
Db       1975 AGAGAAGCTCAAGTCAGAGG 1956


RESULT 6
US-09-400-348-1/c
; Sequence 1, Application US/09400348
; Patent No. 6355778
;  GENERAL INFORMATION:
;    APPLICANT:  Ecker, Joseph
;    APPLICANT:  Alonso, Jose
;    TITLE OF INVENTION:  PLANT GENES FOR SENSITIVITY TO ETHYLENE
;    TITLE OF INVENTION:  AND PATHOGENS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 6355778ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/400,348
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,288
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Beardell, Lori Y.
;      REGISTRATION NUMBER:  34,293
;      REFERENCE/DOCKET NUMBER:  UPN-2949
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-568-3100
;      TELEFAX:  215-568-3439
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6172 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-09-400-348-1

  Query Match             0.5%;  Score 20;  DB 3;  Length 6172;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        966 AGAGAAGCTCAAGTCAGAGG 985
              ||||||||||||||||||||
Db       1975 AGAGAAGCTCAAGTCAGAGG 1956


RESULT 7
US-10-144-198-11
; Sequence 11, Application US/10144198
; Patent No. 6833247
; GENERAL INFORMATION:
;  APPLICANT: OriGene Technologies Inc
;  TITLE OF INVENTION: Regulated Prostate Cance Genes
;  FILE REFERENCE: 9U 105 R1
;  CURRENT APPLICATION NUMBER: US/10/144,198
;  CURRENT FILING DATE:  2002-05-14
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 8733
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (473)..(8566)
US-10-144-198-11

  Query Match             0.5%;  Score 20;  DB 4;  Length 8733;
  Best Local Similarity   100.0%;  Pred. No. 31;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        322 ACAGCAGCAGAGACAGAAGA 341
              ||||||||||||||||||||
Db       8459 ACAGCAGCAGAGACAGAAGA 8478


RESULT 8
US-09-949-016-14371/c
; Sequence 14371, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14371
;   LENGTH: 57837
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-14371

  Query Match             0.5%;  Score 20;  DB 4;  Length 57837;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2398 ACCTCCCCCAGCCTGAAATC 2417
              ||||||||||||||||||||
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Db      19969 ACCTCCCCCAGCCTGAAATC 19950


RESULT 9
US-09-949-016-17601/c
; Sequence 17601, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17601
;   LENGTH: 57839
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-17601

  Query Match             0.5%;  Score 20;  DB 4;  Length 57839;
  Best Local Similarity   100.0%;  Pred. No. 35;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2398 ACCTCCCCCAGCCTGAAATC 2417
             ||||||||||||||||||||
Db      19970 ACCTCCCCCAGCCTGAAATC 19951


RESULT 10
US-09-621-976-2835
; Sequence 2835, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 2835
;   LENGTH: 400
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 99..308
;   NAME/KEY: misc_feature
;   LOCATION: 21
;   OTHER INFORMATION: n=a, g, c or t
US-09-621-976-2835

  Query Match             0.5%;  Score 19;  DB 4;  Length 400;
  Best Local Similarity   100.0%;  Pred. No. 81;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3573 AGCCTGGTCTGAAACTGCT 3591
             |||||||||||||||||||
Db        333 AGCCTGGTCTGAAACTGCT 351


RESULT 11
US-09-949-016-19079
; Sequence 19079, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19079
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-19079

  Query Match             0.5%;  Score 19;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1468 TTCTTCCACCTCAGTCTCC 1486
             |||||||||||||||||||
Db         29 TTCTTCCACCTCAGTCTCC 47


RESULT 12
US-09-949-016-19080
; Sequence 19080, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19080
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-19080

  Query Match             0.5%;  Score 19;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1468 TTCTTCCACCTCAGTCTCC 1486
             |||||||||||||||||||
Db         41 TTCTTCCACCTCAGTCTCC 59


RESULT 13
US-09-949-016-36893
; Sequence 36893, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
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;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36893
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-36893

  Query Match             0.5%;  Score 19;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1468 TTCTTCCACCTCAGTCTCC 1486
              ||||||||||||||||||
Db         29 TTCTTCCACCTCAGTCTCC 47


RESULT 14
US-09-949-016-36894
; Sequence 36894, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36894
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-36894

  Query Match             0.5%;  Score 19;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1468 TTCTTCCACCTCAGTCTCC 1486
              ||||||||||||||||||
Db         41 TTCTTCCACCTCAGTCTCC 59


RESULT 15
US-09-949-016-58788
; Sequence 58788, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58788
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-58788

  Query Match             0.5%;  Score 19;  DB 4;  Length 601;
  Best Local Similarity   100.0%;  Pred. No. 83;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2416 TCTCTGAGCCTGGCAGGAA 2434
              ||||||||||||||||||
Db        147 TCTCTGAGCCTGGCAGGAA 165


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GenCore version 5.1.6

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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4035	100.0	4035	14	US-10-124-498-5	Sequence 5, Appli
2	4035	100.0	4035	14	US-10-066-521-5	Sequence 5, Appli
3	2917	72.3	3489	18	US-10-416-642-3	Sequence 3, Appli
4	2917	72.3	3926	15	US-10-216-645-1	Sequence 1, Appli
5	2862	70.9	3830	15	US-10-216-645-3	Sequence 3, Appli
6	2801	69.4	3226	18	US-10-092-900A-347	Sequence 347, App
7	2713	67.2	3885	20	US-10-860-761-3	Sequence 3, Appli
8	2713	67.2	3900	17	US-10-399-443-23	Sequence 23, Appl
9	2713	67.2	3900	18	US-10-677-943-23	Sequence 23, Appl
10	1102	27.3	1157	17	US-10-399-443-1	Sequence 1, Appli
11	1102	27.3	1157	18	US-10-677-943-1	Sequence 1, Appli
12	657	16.3	1075	17	US-10-399-443-3	Sequence 3, Appli
13	657	16.3	1075	18	US-10-677-943-3	Sequence 3, Appli
14	174	4.3	2099	13	US-10-027-632-258159	Sequence 258159,
15	174	4.3	2099	17	US-10-027-632-258159	Sequence 258159,
c 16	24	0.6	24	17	US-10-399-443-13	Sequence 13, Appl
c 17	24	0.6	24	17	US-10-399-443-14	Sequence 14, Appl
18	24	0.6	24	18	US-10-092-900A-750	Sequence 750, App
c 19	24	0.6	24	18	US-10-677-943-13	Sequence 13, Appl
c 20	24	0.6	24	18	US-10-677-943-14	Sequence 14, Appl
21	22	0.5	22	17	US-10-399-443-7	Sequence 7, Appli
22	22	0.5	22	18	US-10-677-943-7	Sequence 7, Appli
23	22	0.5	26	17	US-10-399-443-9	Sequence 9, Appli
24	22	0.5	26	18	US-10-677-943-9	Sequence 9, Appli
25	22	0.5	27	17	US-10-399-443-17	Sequence 17, Appl
26	22	0.5	27	18	US-10-677-943-17	Sequence 17, Appl
27	22	0.5	1036	20	US-10-739-930-4220	Sequence 4220, Ap
28	22	0.5	3447	17	US-10-399-443-5	Sequence 5, Appli
29	22	0.5	3447	18	US-10-677-943-5	Sequence 5, Appli
30	21	0.5	21	15	US-10-216-645-6	Sequence 6, Appli
c 31	21	0.5	21	15	US-10-216-645-10	Sequence 10, Appl
c 32	21	0.5	21	17	US-10-399-443-8	Sequence 8, Appli
33	21	0.5	21	17	US-10-399-443-19	Sequence 19, Appl
c 34	21	0.5	21	17	US-10-399-443-20	Sequence 20, Appl
35	21	0.5	21	18	US-10-092-900A-749	Sequence 749, App
c 36	21	0.5	21	18	US-10-092-900A-751	Sequence 751, App
c 37	21	0.5	21	18	US-10-677-943-8	Sequence 8, Appli
38	21	0.5	21	18	US-10-677-943-19	Sequence 19, Appl
c 39	21	0.5	21	18	US-10-677-943-20	Sequence 20, Appl
40	21	0.5	21	18	US-10-677-943-41	Sequence 41, Appl
c 41	21	0.5	22	17	US-10-399-443-16	Sequence 16, Appl
c 42	21	0.5	22	18	US-10-677-943-16	Sequence 16, Appl
c 43	21	0.5	476	10	US-09-918-995-6234	Sequence 6234, Ap
c 44	21	0.5	483	10	US-09-918-995-20036	Sequence 20036, A
c 45	21	0.5	495	20	US-10-723-860-2423	Sequence 2423, Ap

ALIGNMENTS

RESULT 1
US-10-124-498-5
; Sequence 5, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4032)
US-10-124-498-5

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  Query Match             100.0%;  Score 4035;  DB 14;  Length 4035;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
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Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
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Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
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Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

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Qy        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360
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Db        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360

Qy        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420
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Db        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420

Qy        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480
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Db        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480

Qy        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540
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Db        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540

Qy        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600
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Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660
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Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

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Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780
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Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840
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Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900
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Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960
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Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080
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Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140
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Qy       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200
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Qy       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260
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Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260

Qy       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320
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Qy       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440
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Qy       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500
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Qy       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
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Qy       2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880
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Qy       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
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Qy       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
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Qy       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
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Db       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
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Qy       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
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Db       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
Qy       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
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Db       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
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Db       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Qy       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
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Db       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
Qy       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
Qy       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
Qy       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
Qy       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
Qy       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
Qy       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
Qy       4021 GGGCTGGTGTCTTAA 4035
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Db       4021 GGGCTGGTGTCTTAA 4035
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RESULT 2
US-10-066-521-5
; Sequence 5, Application US/10066521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-334001
; CURRENT APPLICATION NUMBER: US/10/066,521
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10

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;  PRIOR APPLICATION NUMBER: 60/265,231
;  PRIOR FILING DATE: 2001-01-31
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 4035
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(4032)
US-10-066-521-5.

  Query Match             100.0%;  Score 4035;  DB 14;  Length 4035;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300

Qy        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360

Qy        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420

Qy        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480

Qy        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540

Qy        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

Qy        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140

Qy       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGGAGAGCGTCGCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGGAGAGCGTCGCC 1200

Qy       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260

Qy       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320

Qy       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380

Qy       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440

Qy       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500

Qy       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560

Qy       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620

Qy       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680

Qy       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740

Qy       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800

Qy       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860

Qy       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920

Qy       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
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Db      1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
Qy      1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
Db      1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
Qy      2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Db      2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Qy      2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Db      2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Qy      2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
Db      2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
Qy      2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
Db      2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
Qy      2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
Db      2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
Qy      2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
Db      2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
Qy      2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
Db      2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
Qy      2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520
Db      2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520
Qy      2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
Db      2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
Qy      2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Db      2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Qy      2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Db      2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Qy      2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Db      2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Qy      2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
Db      2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
Qy      2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880
Db      2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880
Qy      2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
Db      2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
Qy      2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
Db      2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
Qy      3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Db      3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Qy      3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
Db      3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
Qy      3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
Db      3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
Qy      3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
Db      3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
Qy      3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
Db      3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
Qy      3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
Db      3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
Qy      3361 GCCTTGCTGTGGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
Db      3361 GCCTTGCTGTGGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
Qy      3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Db      3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Qy      3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
Db      3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
Qy      3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
Db      3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
Qy      3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
Db      3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
Qy      3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
Db      3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
Qy      3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
Db      3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
Qy      3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
Db      3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
Qy      3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
Db      3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
Qy      3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
Db      3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
Qy      3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
Db      3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
Qy      4021 GGGCTGGTGTCTTAA 4035
Db      4021 GGGCTGGTGTCTTAA 4035

RESULT 3
US-10-416-642-3
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; Sequence 3, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  ARVIZU, Chandra
;  TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
;  FILE REFERENCE: PF-0842 PCT
;  CURRENT APPLICATION NUMBER: US/10/416,642
;  CURRENT FILING DATE:  2003-05-13
;  PRIOR APPLICATION NUMBER: 60/249,407
;  PRIOR FILING DATE: 2000-11-15
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PERL Program
; SEQ ID NO 3
;   LENGTH: 3489
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1
US-10-416-642-3

  Query Match             72.3%;  Score 2917;  DB 18;  Length 3489;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 3017;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        290 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAA 511

Qy        350 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 571

Qy        410 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 469
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 631

Qy        470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 691

Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 751

Qy        590 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 649
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCT 811

Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 871

Qy        710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
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Qy        830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
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Db        992 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 1051

Qy        890 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 949
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Qy        950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
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Qy       1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
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RESULT 4
US-10-216-645-1
; Sequence 1, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LESSL, MONIKA
; APPLICANT: PETERS-KOTTIG, MICHAELE
; APPLICANT: BECKMANN, GEORG
; TITLE OF INVENTION: HUMAN MATER PROTEINS
; FILE REFERENCE: SCH-1910
; CURRENT APPLICATION NUMBER: US/10/216,645
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-645-1

Query Match 72.3%; Score 2917; DB 15; Length 3926;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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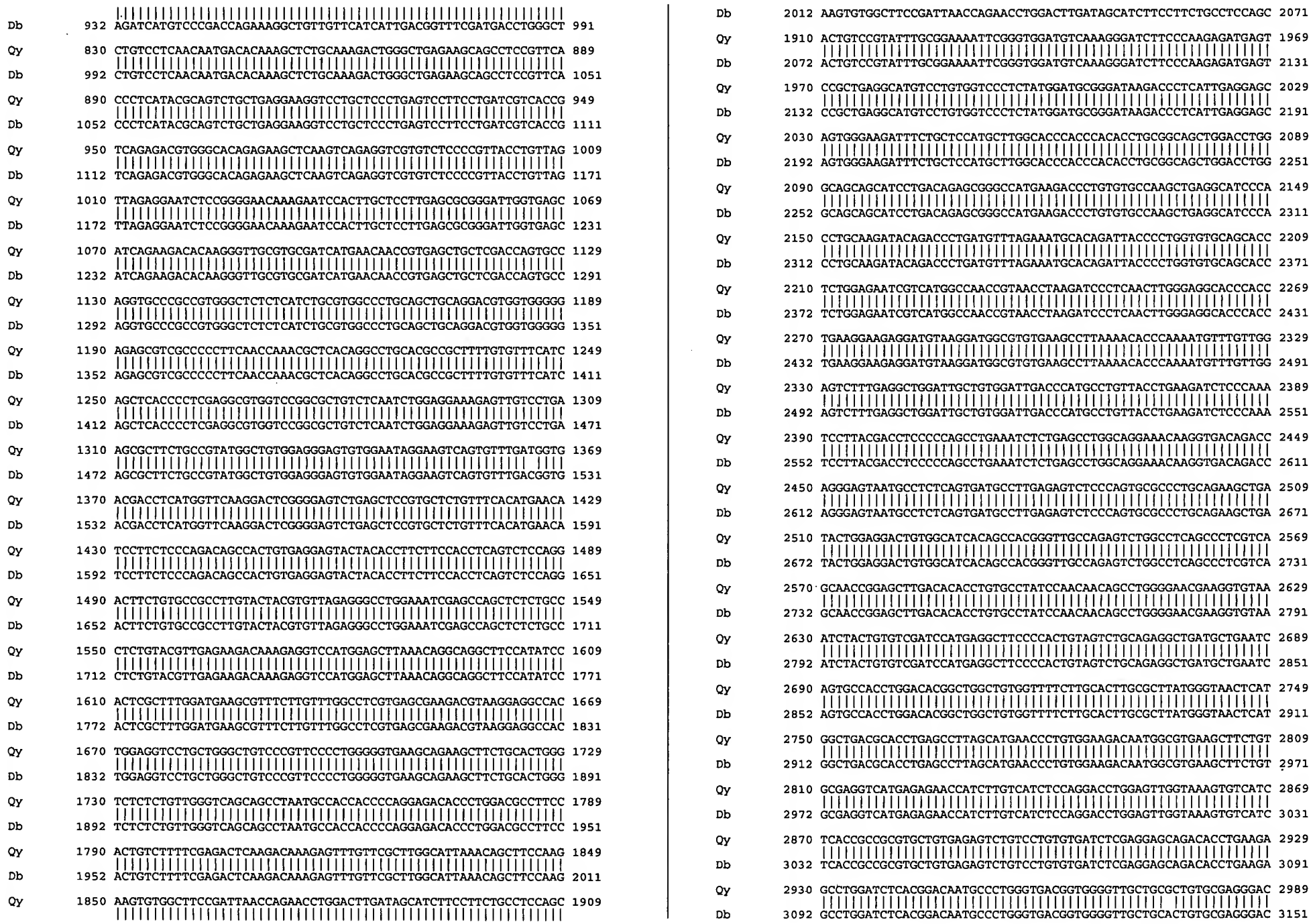
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Qy 2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809
Db 2912 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2971
Qy 2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869
Db 2972 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 3031
Qy 2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929
Db 3032 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 3091
Qy 2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989
Db 3092 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGAC 3151

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Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3152 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3211

Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3212 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3271

Qy       3110 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3272 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3331

Qy       3170 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3332 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3391

Qy       3230 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3289
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Db       3392 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3451

Qy       3290 CTTTTGATGAAGATGACCG 3308
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Db       3452 CTTTTGATGAAGATGACCG 3470


RESULT 5
US-10-216-645-3
; Sequence 3, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
;  APPLICANT: WEISS, BERTRAM
;  APPLICANT:  LESSL, MONIKA
;  APPLICANT:  PETERS-KOTTIG, MICHAELE
;  APPLICANT:  BECKMANN, GEORG
;  TITLE OF INVENTION: HUMAN MATER PROTEINS
;  FILE REFERENCE: SCH-1910
;  CURRENT APPLICATION NUMBER: US/10/216,645
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-216-645-3

  Query Match             70.9%;  Score 2862;  DB 15;  Length 3830;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2962;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        345 AGAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGG 404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 AGAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGG 509

Qy        405 ACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGA 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 ACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGA 569

Qy        465 GGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGC 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        570 GGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGC 629

Qy        525 TGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAA 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 TGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAA 689

Qy        585 GTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGG 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        690 GTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGG 749

Qy        645 ACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAA 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        750 ACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAA 809

Qy        705 GAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGT 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 GAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGT 869

Qy        765 GACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCT 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        870 GACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCT 929

Qy        825 GGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCC 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        930 GGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCC 989

Qy        885 GTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGT 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        990 GTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGT 1049

Qy        945 CACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCT 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 CACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCT 1109

Qy       1005 GTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGG 1064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1110 GTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGG 1169

Qy       1065 TGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCA 1124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1170 TGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCA 1229

Qy       1125 GTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGT 1184
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Db       1230 GTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGT 1289

Qy       1185 GGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTT 1244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1290 GGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTT 1349

Qy       1245 TCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGT 1304
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Db       1350 TCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGT 1409

Qy       1305 CCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGA 1364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1410 CCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGA 1469

Qy       1365 TGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACAT 1424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1470 CGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACAT 1529

Qy       1425 GAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCT 1484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1530 GAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCT 1589

Qy       1485 CCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCT 1544
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1590 CCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCT 1649

Qy       1545 CTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCA 1604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1650 CTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCA 1709

Qy       1605 TATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAG 1664
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1710 TATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAG 1769

Qy       1665 GCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCA 1724
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1770 GCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCA 1829

Qy       1725 CTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGC 1784
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Db       1830 CTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGC 1889

Qy       1785 CTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTT 1844

Db       1890 CTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTT 1949

Qy       1845 CCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCT 1904

Db       1950 CCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCT 2009

Qy       1905 CCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGA 1964

Db       2010 CCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGA 2069

Qy       1965 TGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGA 2024

Db       2070 TGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGA 2129

Qy       2025 GGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGA 2084

Db       2130 GGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGA 2189

Qy       2085 CCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCA 2144

Db       2190 CCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCA 2249

Qy       2145 TCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCA 2204

Db       2250 TCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCA 2309

Qy       2205 GCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCAC 2264

Db       2310 GCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCAC 2369

Qy       2265 CCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTT 2324

Db       2370 CCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTT 2429

Qy       2325 GTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTC 2384

Db       2430 GTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTC 2489

Qy       2385 CCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGAC 2444

Db       2490 CCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGAC 2549

Qy       2445 AGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAA 2504

Db       2550 AGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAA 2609

Qy       2505 GCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCT 2564

Db       2610 GCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCT 2669

Qy       2565 CGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGG 2624

Db       2670 CGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGG 2729

Qy       2625 TGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCT 2684

Db       2730 TGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCT 2789

Qy       2685 GAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAA 2744

Db       2790 GAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAA 2849

Qy       2745 CTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCT 2804

Db       2850 CTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCT 2909

Qy       2805 TCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTG 2864

Db       2910 TCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTG 2969

Qy       2865 TCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCT 2924

Db       2970 TCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCT 3029

Qy       2925 GAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGA 2984

Db       3030 GAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGA 3089

Qy       2985 GGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGAC 3044

Db       3090 GGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGAC 3149

Qy       3045 TTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCT 3104

Db       3150 TTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCT 3209

Qy       3105 AAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGC 3164

Db       3210 AAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGC 3269

Qy       3165 CTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAAT 3224

Db       3270 CTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAAT 3329

Qy       3225 AAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTG 3284

Db       3330 AAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTG 3389

Qy       3285 GCATTCTTTTGATGAAGATGACCG 3308

Db       3390 GCATTCTTTTGATGAAGATGACCG 3413
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RESULT 6
US-10-092-900A-347
; Sequence 347, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev,, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C

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;  CURRENT APPLICATION NUMBER: US/10/092,900A
;  CURRENT FILING DATE:  2002-03-07
;  PRIOR APPLICATION NUMBER: USSN 60/274,322
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/283,675
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: USSN 60/338,092
;  PRIOR FILING DATE: 2001-12-03
;  PRIOR APPLICATION NUMBER: USSN 60/274,281
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/274,191
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/325,681
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: USSN 60/304,354
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: USSN 60/279,995
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: USSN 60/294,899
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: USSN 60/287,424
;  PRIOR FILING DATE: 2001-04-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 347
;   LENGTH: 3226
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (69)..(3168)
US-10-092-900A-347

  Query Match            69.4%;  Score 2801;  DB 18;  Length 3226;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2901;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        406 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 308

Qy        466 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 368

Qy        526 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 428

Qy        586 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 488

Qy        646 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 548

Qy        706 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 765
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 608

Qy        766 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 668

Qy        826 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 728

Qy        886 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 788

Qy        946 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 848

Qy       1006 TTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 1065
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Db        849 TTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 908

Qy       1066 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 968

Qy       1126 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1028

Qy       1186 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1029 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1088

Qy       1246 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1148

Qy       1306 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAT 1365
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Db       1149 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAC 1208

Qy       1366 GGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATG 1425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 GGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATG 1268

Qy       1426 AACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTC 1485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 AACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTC 1328

Qy       1486 CAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTC 1545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 CAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTC 1388

Qy       1546 TGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCAT 1605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1389 TGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCAT 1448

Qy       1606 ATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGG 1665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1449 ATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGG 1508

Qy       1666 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1725
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Db       1509 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1568

Qy       1726 TGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCC 1785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1569 TGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCC 1628

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Db       1629 TTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTC 1688

Qy       1846 CAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTC 1905
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Db       1689 CAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTC 1748

Qy       1906 CAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGAT 1965
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Db       1749 CAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGAT 1808

Qy       1966 GAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAG 2025
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Qy       2026 GAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGAC 2085
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Db       1869 GAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGAC 1928

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Qy       2146 CCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAG 2205
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Qy       2206 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2265
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Qy       2266 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2325
Db       2109 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2168

Qy       2326 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2385
Db       2169 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2228

Qy       2386 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2445
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Qy       2446 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAG 2505
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Qy       2566 GTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGT 2625
Db       2409 GTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGT 2468

Qy       2626 GTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTG 2685
Db       2469 GTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTG 2528

Qy       2686 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2745
Db       2529 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2588

Qy       2746 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2805
Db       2589 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2648

Qy       2806 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2865
Db       2649 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2708

Qy       2866 CATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTG 2925
Db       2709 CATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTG 2768

Qy       2926 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAG 2985
Db       2769 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAG 2828

Qy       2986 GGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACT 3045
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Qy       3046 TCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTA 3105
Db       2889 TCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTA 2948

Qy       3106 AACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCC 3165
Db       2949 AACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCC 3008

Qy       3166 TGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATA 3225
Db       3009 TGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATA 3068

Qy       3226 AGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGG 3285
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Qy       3286 CATTCTTTTGATGAAGATGACCG 3308
Db       3129 CATTCTTTTGATGAAGATGACCG 3151
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RESULT 7
US-10-860-761-3
; Sequence 3, Application US/10860761
; Publication No. US20040248775A1
; GENERAL INFORMATION:
; APPLICANT: WYETH
; TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS
; FILE REFERENCE: AM101318
; CURRENT APPLICATION NUMBER: US/10/860,761
; CURRENT FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 3885
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3603)
US-10-860-761-3

Query Match 67.2%; Score 2713; DB 20; Length 3885;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3013; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        350 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 409
Db        626 TTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATG 685

Qy        410 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 469
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Qy        470 TACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTG 529
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Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
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Qy        710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
Db        986 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 1045

Qy        770 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 829
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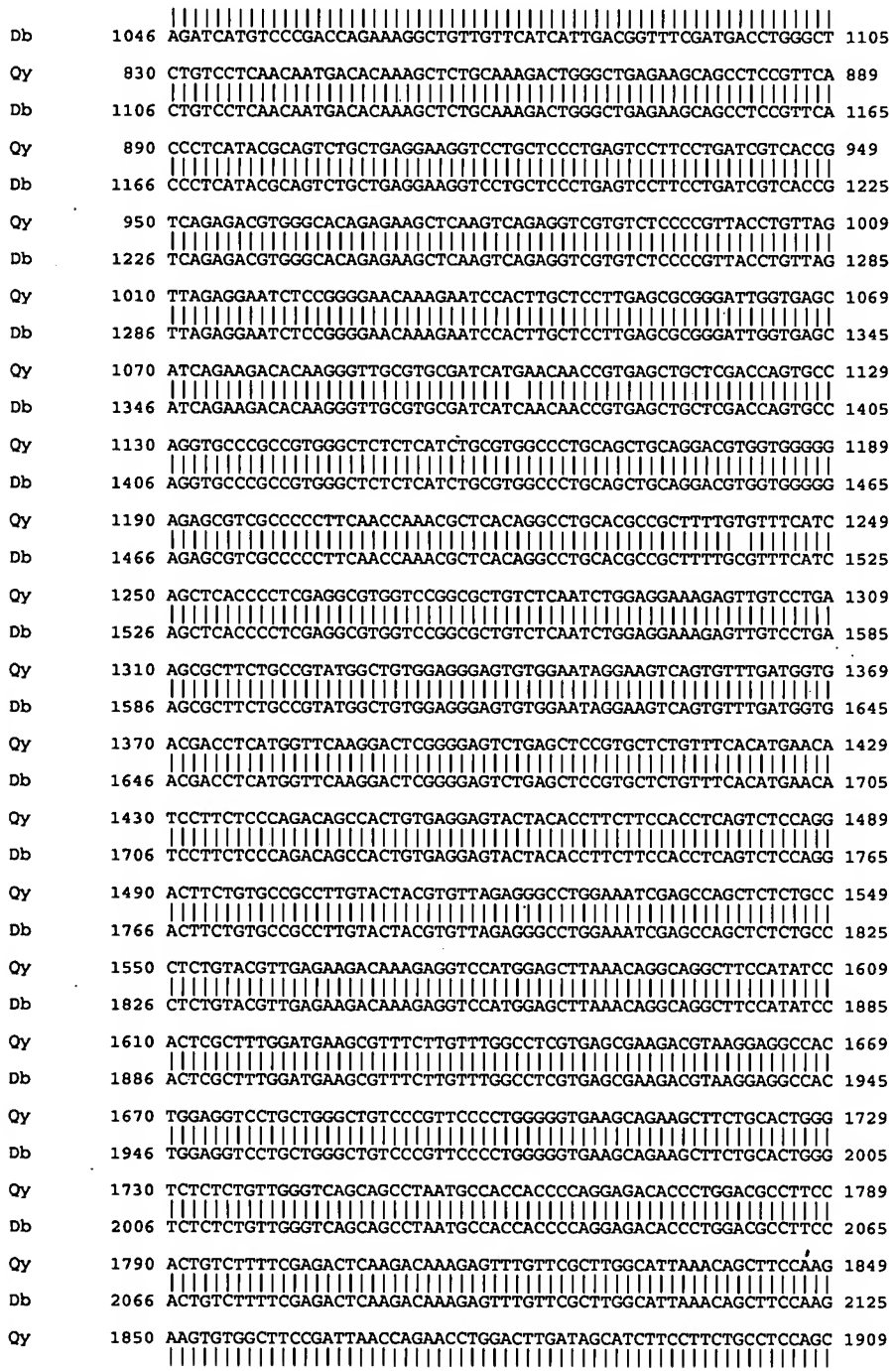
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Db 1106 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 1165
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Qy 950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
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Qy 1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
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Qy 1310 AGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTG 1369
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Qy 1430 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1489
Db 1706 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1765
Qy 1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
Db 1766 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1825
Qy 1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
Db 1826 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1885
Qy 1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
Db 1886 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1945
Qy 1670 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1729
Db 1946 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 2005
Qy 1730 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 1789
Db 2006 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 2065
Qy 1790 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 1849
Db 2066 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 2125
Qy 1850 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 1909
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Db 2186 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 2245
Qy 1970 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2029
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Qy 2030 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2089
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Qy 2270 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2329
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Qy 2390 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2449
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Qy 2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509
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Qy 2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629
Db 2846 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2905
Qy 2630 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2689
Db 2906 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2965
Qy 2690 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 2749
Db 2966 AGTGCCACCTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCAT 3025
Qy 2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809
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Qy 2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869
Db 3086 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 3145
Qy 2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929
Db 3146 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 3205
Qy 2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989
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Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
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Db       3266 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3325

Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
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RESULT 8
US-10-399-443-23
; Sequence 23, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
; OTHER INFORMATION:
US-10-399-443-23

Query Match 67.2%; Score 2713; DB 17; Length 3900;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3013; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db        686 GAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATG 745

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Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
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Db        926 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 985

Qy        710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
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Qy        770 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 829
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Db       1046 AGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCT 1105

Qy        830 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 889
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Db       1106 CTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCA 1165

Qy        890 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 949
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1166 CCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCG 1225

Qy        950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1226 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1285

Qy       1010 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1069
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1286 TTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGC 1345

Qy       1070 ATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCC 1129
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1346 ATCAGAAGACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCC 1405

Qy       1130 AGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGG 1189
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Qy       1190 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATC 1249
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Db       1466 AGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATC 1525

Qy       1250 AGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGA 1309
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Qy       1430 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1489
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Db       1706 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1765

Qy       1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
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Qy       1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
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Qy       1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
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Db       1886 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1945

Qy       1670 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 1729
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Db       1946 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 2005

Qy       1730 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 1789
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Db       2066 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 2125

Qy       1850 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 1909
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Db       2126.AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 2185

Qy       1910 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 1969
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Qy       1970 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2029
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Db       2246 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2305

Qy       2030 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2089
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Qy       2090 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2149
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Qy       2150 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2209
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Db       2426 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACC 2485

Qy       2210 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2269
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Db       2486 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2545

Qy       2270 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2329
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Qy       2330 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2389
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Qy       2390 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2449
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Qy       2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509
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Qy       2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629
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Db       2846 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2905

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Qy       2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809
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Db       3026 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 3085

Qy       2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869
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Db       3086 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 3145

Qy       2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929
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Db       3146 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 3205

Qy       2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989
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Db       3206 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 3265

Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
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Db       3266 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3325

Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
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Db       3326 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3385

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Db       3566 CTTTTGATGAAGATGACCG 3584
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RESULT 9
US-10-677-943-23
; Sequence 23, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA

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;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3600)
US-10-677-943-23

  Query Match            67.2%;  Score 2713;  DB 18;  Length 3900;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 3013;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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Qy        530 CTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAG 589
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Qy        650 ACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGG 709
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Qy        710 AGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGG 769
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Qy        950 TCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAG 1009
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Db       1646 ACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACA 1705

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Db       1706 TCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGG 1765

Qy       1490 ACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCC 1549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1550 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1609
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Db       1826 CTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCC 1885

Qy       1610 ACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCAC 1669
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Db       1946 TGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGG 2005

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Db       2006 TCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCC 2065

Qy       1790 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 1849
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Db       2066 ACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAG 2125

Qy       1850 AAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGC 1909
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Qy       1910 ACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGT 1969
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Db       2246 CCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGC 2305

Qy       2030 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2089
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2306 AGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGG 2365

Qy       2090 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2366 GCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCA 2425

Qy       2150 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACC 2209
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db       2426 CCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACC 2485

Qy       2210 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2269
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2486 TCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACC 2545

Qy       2270 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2329
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2546 TGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGG 2605
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Qy       2330 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2389
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2606 AGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAA 2665

Qy       2390 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2449
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2666 TCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACC 2725

Qy       2450 AGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2509
             ||||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||
Db       2726 AGGGAGTAACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGA 2785

Qy       2510 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2569
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2786 TACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCA 2845

Qy       2570 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2629
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2846 GCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAA 2905

Qy       2630 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2689
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2906 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATC 2965

Qy       2690 AGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCAT 2749
             ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2966 AGTGCCACCTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCAT 3025

Qy       2750 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 2809
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3026 GGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGT 3085

Qy       2810 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 2869
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3086 GCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATC 3145

Qy       2870 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 2929
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3146 TCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGA 3205

Qy       2930 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 2989
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3206 GCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGAC 3265

Qy       2990 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3049
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3266 TGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTG 3325

Qy       3050 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3109
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3326 ATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACC 3385

Qy       3110 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3169
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3386 TGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTC 3445

Qy       3170 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3229
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3446 CCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGA 3505

Qy       3230 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3289
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3506 AGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATT 3565

Qy       3290 CTTTTGATGAAGATGACCG 3308
             ||||||||||||||||||||
Db       3566 CTTTTGATGAAGATGACCG 3584


RESULT 10
US-10-399-443-1
; Sequence 1, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute
;  APPLICANT:  Health
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-399-443-1

  Query Match             27.3%;  Score 1102;  DB 17;  Length 1157;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1152;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        757 GCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTC 816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTC 63

Qy        817 GATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 123

Qy        877 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 183

Qy        937 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 996
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 243

Qy        997 CGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGC 1056
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGC 303

Qy       1057 GGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTG 1116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 GGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTG 363

Qy       1117 CTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAG 1176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAG 423

Qy       1177 GACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCT 1236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCT 483

Qy       1237 TTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAA 1296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAA 543

Qy       1297 AGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCA 1356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCA 603

Qy       1357 GTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTG 1416
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 GTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTG 663

Qy       1417 TTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCAC 1476
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Db        664 TTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCAC 723

Qy       1477 CTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAG 1536
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 CTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAG 783

Qy       1537 CCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCA 1596
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 CCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCA 843

Qy       1597 GGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGAC 1656
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 GGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGAC 903

Qy       1657 GTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAG 1716
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 GTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAG 963

Qy       1717 CTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACC 1776
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 CTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACC 1023

Qy       1777 CTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTA 1836
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 CTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTA 1083

Qy       1837 AACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCC 1896
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 AACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCC 1143

Qy       1897 TTCTGCCTCCAGC 1909
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Db       1144 TTCTGCCTCCAGC 1156


RESULT 11
US-10-677-943-1
; Sequence 1, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-677-943-1

  Query Match             27.3%;  Score 1102;  DB 18;  Length 1157;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1152;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        757 GCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTC 816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 GCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTC 63

Qy        817 GATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 GATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 123

Qy        877 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         124 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 183

Qy        937 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 996
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         184 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 243

Qy        997 CGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGC 1056
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         244 CGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGC 303

Qy       1057 GGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTG 1116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         304 GGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTG 363

Qy       1117 CTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAG 1176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         364 CTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAG 423

Qy       1177 GACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCT 1236
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         424 GACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCT 483

Qy       1237 TTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAA 1296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         484 TTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAA 543

Qy       1297 AGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCA 1356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         544 AGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCA 603

Qy       1357 GTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTG 1416
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         604 GTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTG 663

Qy       1417 TTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCAC 1476
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         664 TTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCAC 723

Qy       1477 CTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAG 1536
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         724 CTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAG 783

Qy       1537 CCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCA 1596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         784 CCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCA 843

Qy       1597 GGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGAC 1656
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         844 GGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGAC 903

Qy       1657 GTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAG 1716
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         904 GTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAG 963

Qy       1717 CTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACC 1776
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         964 CTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACC 1023

Qy       1777 CTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTA 1836
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1024 CTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTA 1083

Qy       1837 AACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCC 1896
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1084 AACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCC 1143

Qy       1897 TTCTGCCTCCAGC 1909
              |||||||||||||
Db        1144 TTCTGCCTCCAGC 1156
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Db       1144 TTCTGCCTCCAGC 1156


RESULT 12
US-10-399-443-3
; Sequence 3, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute
;  APPLICANT:  Health
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1075
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-399-443-3

  Query Match             16.3%;  Score 657;  DB 17;  Length 1075;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  757;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2550 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 2609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 60

Qy       2610 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 2669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 120

Qy       2670 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACT 2729
             ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        121 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTCTCTTGCACT 180

Qy       2730 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 2789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 240

Qy       2790 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 2849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 300

Qy       2850 GGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 2909
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Db        301 GGAGTTGGTAAAATGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 360

Qy       2910 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 2969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 420

Qy       2970 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 3029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 480

Qy       3030 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 3089
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 540

Qy       3090 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 3149
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 600

Qy       3150 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 3209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 660

Qy       3210 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 3269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 720

Qy       3270 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 3308
             |||||||||||||||||||||||||||||||||||||||
Db        721 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 759


RESULT 13
US-10-677-943-3
; Sequence 3, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 1075
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-677-943-3

  Query Match             16.3%;  Score 657;  DB 18;  Length 1075;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches  757;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2550 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 2609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 60

Qy       2610 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 2669
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 120

Qy       2670 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACT 2729
             ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        121 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTCTCTTGCACT 180

Qy       2730 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 2789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 240

Qy       2790 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 2849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 300

Qy       2850 GGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 2909
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGTTGGTAAAATGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 360

Qy       2910 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 2969
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        361 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 420

Qy       2970 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 3029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 480

Qy       3030 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 3089
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Qy       3090 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 3149
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Db        541 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 600

Qy       3150 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 3209
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Db        601 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 660

Qy       3210 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 3269
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 720

Qy       3270 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 3308
             |||||||||||||||||||||||||||||||||||||||
Db        721 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 759


RESULT 14
US-10-027-632-258159
; Sequence 258159, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 258159
;   LENGTH: 2099
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-258159

  Query Match             4.3%;  Score 174;  DB 13;  Length 2099;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-80;
  Matches  174;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2000 GGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCA 2059
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 GGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCA 277

Qy       2060 CCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGA 2119
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 CCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGA 337

Qy       2120 AGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGT 2173
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 AGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGT 391


RESULT 15
US-10-027-632-258159
; Sequence 258159, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 258159
;   LENGTH: 2099
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-258159

  Query Match             4.3%;  Score 174;  DB 17;  Length 2099;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-80;
  Matches  174;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2000 GGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCA 2059
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Db        218 GGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCA 277

Qy       2060 CCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGA 2119
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 CCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGA 337

Qy       2120 AGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGT 2173
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Db        338 AGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGT 391


Search completed: July 19, 2005, 12:03:16
Job time : 2599 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 01:37:21 ; Search time 12239 Seconds
(without alignments)
12549.173 Million cell updates/sec

Title: US-10-066-521-5
Perfect score: 4035
Sequence: 1 atggaaggagacaaatcgct.....tcgaggggctggtgtcttaa 4035

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	679	16.8	791	7	CK000513	CK000513 AGENCOURT
c	2	322	8.0	693	5	BU634350	BU634350 UI-H-FL1-
c	3	299	7.4	684	5	BU630481	BU630481 UI-H-FL0-
c	4	256	6.3	642	5	BU618831	BU618831 UI-H-FH1-
c	5	116	2.9	526	8	AQ542616	AQ542616 RPCI-11-3
	6	60	1.5	523	8	AQ428788	AQ428788 CITBI-E1-
	7	58	1.4	814	6	CB228956	CB228956 AGENCOURT
c	8	50	1.2	743	9	AG117567	AG117567 Pan trogl
c	9	24	0.6	917	2	BF133827	BF133827 601778752
	10	23	0.6	827	9	CR182764	CR182764 Reverse s
c	11	22	0.5	308	7	CO311900	CO311900 EK227159.
	12	22	0.5	392	2	BE406212	BE406212 WHE0408_e
	13	22	0.5	394	7	CF916020	CF916020 B0988G02-
	14	22	0.5	407	6	CB807101	CB807101 AMGNNUC:S
	15	22	0.5	425	2	BE406757	BE406757 WHE0406_e
	16	22	0.5	511	7	CF173704	CF173704 B0927G04-
	17	22	0.5	533	6	CA559680	CA559680 K0261H12-
	18	22	0.5	539	2	AW948258	AW948258 RC0-MT001
	19	22	0.5	546	6	CA561388	CA561388 K0286C11-
	20	22	0.5	546	7	CK546518	CK546518 rswhb0_01
	21	22	0.5	559	6	CA561556	CA561556 K0288H05-
	22	22	0.5	583	6	CA559979	CA559979 K0266B01-
	23	22	0.5	585	8	AQ515975	AQ515975 HS_5240_A
	24	22	0.5	589	6	CA559886	CA559886 K0264H01-
	25	22	0.5	593	6	CA558845	CA558845 K0250F09-
	26	22	0.5	599	7	CF915731	CF915731 B0984E03-
c	27	22	0.5	605	7	CK516658	CK516658 rswjb0_00
c	28	22	0.5	625	6	CD338591	CD338591 StrPu537.
	29	22	0.5	636	7	CF914959	CF914959 B0971H02-
	30	22	0.5	643	7	CF913803	CF913803 B0954D05-
	31	22	0.5	666	1	AV367637	AV367637 AV367637
c	32	22	0.5	719	7	CO806156	CO806156 AGENCOURT
c	33	22	0.5	768	7	CO808001	CO808001 AGENCOURT
	34	22	0.5	798	2	BE643252	BE643252 Cri2_8_F0
c	35	22	0.5	835	4	BI957125	BI957125 HVSMEn000
	36	22	0.5	1096	4	BG324013	BG324013 602422255
	37	22	0.5	1119	4	BM454123	BM454123 AGENCOURT
	38	22	0.5	1913	3	AK016782	AK016782 Mus muscu
	39	22	0.5	3475	3	AK087774	AK087774 Mus muscu
c	40	21	0.5	395	1	AA316487	AA316487 EST188400
c	41	21	0.5	412	6	CB126685	CB126685 K-EST0175
c	42	21	0.5	419	7	CN265231	CN265231 170006000
	43	21	0.5	444	2	AW439360	AW439360 xt11h09.x
c	44	21	0.5	456	7	CO380162	CO380162 FRA3426 S
	45	21	0.5	459	1	AI056454	AI056454 oy77a10.x

ALIGNMENTS

RESULT 1
CK000513
LOCUS CK000513 791 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT_16368905 NIH_MGC_221 Homo sapiens cDNA clone IMAGE:30708637 5', mRNA sequence.
ACCESSION CK000513
VERSION CK000513.1 GI:38526547
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 791)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM1075 row: c column: 14
High quality sequence stop: 688.
FEATURES Location/Qualifiers
source 1. .791
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30708637"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_221"
/note="Organ: mixed; Vector: pYX-Asc; Site_1: EcoRI; Site_2: NotI; Library is oligo-dT primed and directionally cloned Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according tomRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pYX-Asc vector. Average insert size 4-5Kb. Adaptors 5'(AATTCGGCACGAGG)3' and 5'd

(CCTCGTGCCG)3'. 3' Linker sequence - GCGGCCGCTGAGAGCC T18. Sequencing primers 3'end: T3 promoter primer 5'd (ATTAACCCTCACTAAAGGGA)3'. 5' End: T7 promoter primer 5'd (TAATACGACTCACTATAGGG)3'. Library was constructed in the laboratory of M. Bento Soares. Note: this is a NIH_MGC Library"

ORIGIN

Query Match 16.8%; Score 679; DB 7; Length 791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        567 GGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCT 626
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Db          7 GGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCT 66

Qy        627 GTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGT 686
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Db         67 GTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGT 126

Qy        687 TAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCC 746
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Db        127 TAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCC 186

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Db        187 AGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCAT 246

Qy        807 TGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTG 866
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Db        247 TGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTG 306

Qy        867 GGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCC 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCC 366

Qy        927 TGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGT 986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 TGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGT 426

Qy        987 CGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCT 1046
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Db        427 CGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCT 486

Qy       1047 CCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAA 1106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 CCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAA 546

Qy       1107 CCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCT 1166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCT 606

Qy       1167 GCAGCTGCAGGACGTGGTGGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCT 1226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 GCAGCTGCAGGACGTGGTGGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCT 666

Qy       1227 GCACGCCGCTTTTGTGTTT 1245
              ||||||||||||||||||
Db        667 GCACGCCGCTTTTGTGTTT 685
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RESULT 2
BU634350/c

```
LOCUS       BU634350                693 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  UI-H-FL1-bgx-m-16-0-UI.s1 NCI_CGAP_FL1 Homo sapiens cDNA clone
            UI-H-FL1-bgx-m-16-0-UI 3', mRNA sequence.
ACCESSION   BU634350
VERSION     BU634350.1  GI:23301605
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 693)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .693
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FL1-bgx-m-16-0-UI"
                     /tissue_type="Cell lines"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FL1"
                     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_FL1 is a normalized cDNA library
                     derived from a pool of mRNA obtained from 4 cell lines
                     from grade III chondrosarcoma tissues. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site.  Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GAGGTCGGTG. The cell lines were provided by Dr. James
                     Martin from the University of Iowa.
                     TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
                     TAG_LIB=UI-H-FL1
                     TAG_SEQ=GAGGTCGGTG"
ORIGIN
```

Query Match 8.0%; Score 322; DB 5; Length 693;
Best Local Similarity 100.0%; Pred. No. 8e-160;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2987 GACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTT 3046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 GACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTT 585

Qy       3047 CTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAA 3106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 CTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAA 525

Qy       3107 ACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCT 3166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 ACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCT 465

Qy       3167 GTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAA 3226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAA 405

Qy       3227 GGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGC 3286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGC 345

Qy       3287 ATTCTTTTGATGAAGATGACCG 3308
              |||||||||||||||||||||
Db        344 ATTCTTTTGATGAAGATGACCG 323
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RESULT 3
BU630481/c
LOCUS       BU630481                684 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  UI-H-FL0-bdk-c-22-0-UI.s1 NCI_CGAP_FL0 Homo sapiens cDNA clone
            UI-H-FL0-bdk-c-22-0-UI 3', mRNA sequence.
ACCESSION   BU630481
VERSION     BU630481.1  GI:23297486
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 684)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .684
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FL0-bdk-c-22-0-UI"
                     /tissue_type="Cell lines"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FL0"
                     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_FL0 is a cDNA library derived from
                     a pool of mRNA obtained from 4 cell lines from grade III
                     chondrosarcoma tissues. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is GAGGTCGGTG. The cell line
                     was provided by Dr James Martin from University of Iowa.
                     TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
                     TAG_LIB=UI-H-FL0
                     TAG_SEQ=GAGGTCGGTG"
ORIGIN

  Query Match             7.4%;  Score 299;  DB 5;  Length 684;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-147;
  Matches  299;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2966 GGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGT 3025
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 GGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGT 599

Qy       3026 TGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCA 3085
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         598 TGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCA 539

Qy       3086 ACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGA 3145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         538 ACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGA 479

Qy       3146 AGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAAT 3205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         478 AGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAAT 419

Qy       3206 GGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGA 3264
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         418 GGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGA 360


RESULT 4
BU618831/c
LOCUS       BU618831                642 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  UI-H-FH1-bfl-i-19-0-UI.s1 NCI_CGAP_FH1 Homo sapiens cDNA clone
            UI-H-FH1-bfl-i-19-0-UI 3', mRNA sequence.
ACCESSION   BU618831
VERSION     BU618831.1  GI:23285046
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .642
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FH1-bfl-i-19-0-UI"
                     /tissue_type="Cell Line"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FH1"
                     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_FH1 is a normalized cDNA library
                     obtained from a cell line derived from grade I
                     chondrosarcoma tissue. The library was constructed and
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     AGAATCCGGC. The cell line was provided by Dr. James Martin
                     from the University of Iowa.
                     TAG_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
                     Chondrosarcoma
                     TAG_LIB=UI-H-FH1
                     TAG_SEQ=AGAATCCGGC"
ORIGIN

  Query Match             6.3%;  Score 256;  DB 5;  Length 642;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-124;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy       3009 TCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTC 3068
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 TCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTC 556

Qy       3069 CTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAG 3128
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         555 CTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAG 496

Qy       3129 TCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGAT 3188
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         495 TCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGAT 436

Qy       3189 AATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCA 3248
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         435 AATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCA 376

Qy       3249 GCTACTCAAGCCCCGA 3264
             ||||||||||||||||
Db         375 GCTACTCAAGCCCCGA 360
```

```
RESULT 5
AQ542616/c
LOCUS       AQ542616                526 bp    DNA     linear   GSS 19-MAY-1999
DEFINITION  RPCI-11-345A9.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-345A9,
            genomic survey sequence.
ACCESSION   AQ542616
VERSION     AQ542616.1  GI:4873072
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 526)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: RPCI-11-345A9.TV
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .526
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="GDB:7632104"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-345A9"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /clone_lib="RPCI-11"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
ORIGIN

  Query Match             2.9%;  Score 116;  DB 8;  Length 526;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-49;
  Matches  116;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2516 AGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACC 2575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 AGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACC 243

Qy       2576 GGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAAT 2631
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         242 GGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAAT 187
```

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RESULT 6
AQ428788
LOCUS       AQ428788                523 bp    DNA     linear   GSS 24-MAR-1999
DEFINITION  CITBI-E1-2560I17.TF CITBI-E1 Homo sapiens genomic clone 2560I17,
            genomic survey sequence.
ACCESSION   AQ428788
VERSION     AQ428788.1  GI:4496554
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 523)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2560I17.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .523
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="2560I17"
                     /sex="male"
                     /cell_type="sperm"
                     /clone_lib="CITBI-E1"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
ORIGIN

  Query Match             1.5%;  Score 60;  DB 8;  Length 523;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-19;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        345 AGAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGG 404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 AGAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGG 80
```

```
RESULT 7
CB228956
LOCUS       CB228956                814 bp    mRNA    linear   EST 10-FEB-2003
DEFINITION  AGENCOURT_11501187 NICHD_Rh_Ov1 Macaca mulatta cDNA clone
            IMAGE:6884760 5', mRNA sequence.
ACCESSION   CB228956
VERSION     CB228956.1  GI:28280534
KEYWORDS    EST.
SOURCE      Macaca mulatta (rhesus monkey)
  ORGANISM  Macaca mulatta
```

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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 814)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Eliot Spindel
             cDNA Library Preparation: CLONTECH
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM3135  row: b  column: 23
            High quality sequence stop: 235.
FEATURES             Location/Qualifiers
     source          1. .814
                     /organism="Macaca mulatta"
                     /mol_type="mRNA"
                     /db_xref="taxon:9544"
                     /clone="IMAGE:6884760"
                     /tissue_type="Ovary"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHD_Rh_Ov1"
                     /note="Organ: ovary; Vector: pDNR-LIB; Site_1: Sfi I;
                     Site_2: Sfi I; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.0-4.0 kb. Tissue pooled from
                     pre-pubertal, post pubertal sn menopausal monkeys.
                     Constructed by Clontech. Note: this is a NICHD Library."
ORIGIN

  Query Match             1.4%;  Score 58;  DB 6;  Length 814;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-18;
  Matches   58;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2289 GATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGAT 2346
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 GATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGAT 197


RESULT 8
AG117567/c
LOCUS       AG117567                743 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-125H04.F, genomic survey sequence.
ACCESSION   AG117567
VERSION     AG117567.1  GI:16738086
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 743)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                Sequencing: -21M13
            LIBRARY
                Vector    : pKS145
                R.Site 1  : SacI
                R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .743
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="PTB-125H04.F"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN

  Query Match             1.2%;  Score 50;  DB 9;  Length 743;
  Best Local Similarity   100.0%;  Pred. No. 3e-14;
  Matches   50;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3332 GGCTCCCTGAAAGCCGGGCATGGCCATGTGCCTTGCTGTGGGGGATGAAC 3381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 GGCTCCCTGAAAGCCGGGCATGGCCATGTGCCTTGCTGTGGGGGATGAAC 247


RESULT 9
BF133827/c
LOCUS       BF133827                917 bp    mRNA    linear   EST 24-OCT-2000
DEFINITION  601778752F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4006716 5',
            mRNA sequence.
ACCESSION   BF133827
VERSION     BF133827.1  GI:10972867
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 917)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by:Incyte Genomics, Inc.
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9238  row: h  column: 13
            High quality sequence stop: 630.
FEATURES             Location/Qualifiers
     source          1. .917
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="CZECH II"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4006716"
                     /tissue_type="tumor, metastatic to mammary"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu30"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; transgenic model WNT-1, expression driven by
                     MMTV-LTR enhancer; Cloned unidirectionally.  Primer: Oligo
                     dT.   Library constructed by Life Technologies.
                     Investigator providing samples: Gilbert Smith, NIH"
ORIGIN

  Query Match             0.6%;  Score 24;  DB 2;  Length 917;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy       1895 CCTTCTGCCTCCAGCACTGTCCGT 1918
              ||||||||||||||||||||||||
Db        742 CCTTCTGCCTCCAGCACTGTCCGT 719


RESULT 10
CR182764
LOCUS       CR182764                827 bp    DNA     linear   GSS 06-JUL-2004
DEFINITION  Reverse strand read from insert in 5'HPRT insertion targeting and
            chromosome engineering clone MHPN374o02, genomic survey sequence.
ACCESSION   CR182764
VERSION     CR182764.1  GI:49961613
KEYWORDS    GSS; genome survey sequence; MICER.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 827)
  AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES             Location/Qualifiers
     source          1. .827
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
                     /clone="MHPN374o02"
                     /clone_lib="MHPN"
ORIGIN

  Query Match             0.6%;  Score 23;  DB 9;  Length 827;
  Best Local Similarity   100.0%;  Pred. No. 8.7;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2977 CTGTGCGAGGGACTGAAGCAAAA 2999
              |||||||||||||||||||||||
Db         49 CTGTGCGAGGGACTGAAGCAAAA 71


RESULT 11
CO311900/c
LOCUS       CO311900                308 bp    mRNA    linear   EST 28-JUN-2004
DEFINITION  EK227159.5prime Exelixis FlyTag CK01 pCDNA-SK+ Drosophila
            melanogaster cDNA clone EK227159 5, mRNA sequence.
ACCESSION   CO311900
VERSION     CO311900.1  GI:49366701
KEYWORDS    EST.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 308)
  AUTHORS   Kopczynski,C., Platt,D., Campbell,J., Muzong,C., Laufer,A.,
            Peterson,E. and Swimmer,C.
  TITLE     Exelixis FlyTag EST Project CK01 Library
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: EK.2271  row: E  column: 11
            High quality sequence stop: 267.
FEATURES             Location/Qualifiers
     source          1. .308
                     /organism="Drosophila melanogaster"
                     /mol_type="mRNA"
                     /db_xref="taxon:7227"
                     /clone="EK227159"
                     /clone_lib="Exelixis FlyTag CK01 pCDNA-SK+"
                     /note="Organ: mixed stage embryos, imaginal disks, and
                     adult heads; Vector: pCDNA-SK+; Site_1: NotI; Site_2:
                     XhoI; Random primed, normalized library from mixed stage
                     embryos, imaginal disks, and adult heads."
ORIGIN

  Query Match             0.5%;  Score 22;  DB 7;  Length 308;
  Best Local Similarity   100.0%;  Pred. No. 27;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2553 GGCCTCAGCCCTCGTCAGCAAC 2574
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Db        201 GGCCTCAGCCCTCGTCAGCAAC 180


RESULT 12
BE406212
LOCUS       BE406212                392 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  WHE0408_e11_e11zB Wheat etiolated seedling root cDNA library
            Triticum aestivum cDNA clone WHE0408_e11_e11, mRNA sequence.
ACCESSION   BE406212
VERSION     BE406212.1  GI:9365680
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D.,
            Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
            Seaton,C.L. and Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Strategene pBluescript SK reverse primer.
FEATURES             Location/Qualifiers
     source          1. .392
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE0408_e11_e11"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Wheat etiolated seedling root cDNA library"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RNA, and
                     poly(A) RNA were prepared, a cDNA library  was made, and
                     the cDNA clones were in vivo excised to give pBluescript
                     phagemids in the TJ Close lab (Choi, Close, Fenton) at the
                     University  of California, Riverside.  Plasmid DNA
                     preparations and DNA sequencing  were performed in the OD
                     Anderson lab (all other authors)."
ORIGIN

  Query Match             0.5%;  Score 22;  DB 2;  Length 392;
```

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  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1482 TCTCCAGGACTTCTGTGCCGCC 1503
              ||||||||||||||||||||||
Db        162 TCTCCAGGACTTCTGTGCCGCC 183


RESULT 13
CF916020
LOCUS       CF916020                394 bp    mRNA    linear   EST 05-NOV-2003
DEFINITION  B0988G02-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
            musculus cDNA clone NIA:B0988G02 IMAGE:30480745 5', mRNA sequence.
ACCESSION   CF916020
VERSION     CF916020.1  GI:38187222
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 394)
  AUTHORS   Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
  TITLE     Construction of long-transcript enriched cDNA libraries from
            submicrogram amounts of total RNAs by a universal PCR amplification
            method
  JOURNAL   Genome Res. 11 (9), 1553-1558 (2001)
  MEDLINE   21429098
   PUBMED   11544199
COMMENT     Contact: Dawood B. Dudekula
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            Plate: B0988  row: G  column: 02
            Seq primer: M13 Reverse
            High quality sequence stop: 394
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .394
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="niaEST:B0988G02-5"
                     /db_xref="taxon:10090"
                     /clone="NIA:B0988G02 IMAGE:30480745"
                     /dev_stage="Unfertilized Egg"
                     /lab_host="DH10B"
                     /clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                     1)"
                     /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                     Site_2: NotI; Mouse cDNA project by the Laboratory of
                     Genetics, National Institute on Aging (NIA), Intramural
                     Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
                     This is a long-transcript enriched cDNA library (Ref.
                     Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
                     RNAs were extracted from a pool of 1488 unfertilized eggs.
                     Double-stranded cDNAs were synthesized with an Oligo(dT)
                     primer [Invitrogen:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT-3'],
                     treated with T4 DNA polymerase, and purified by
                     ethanol-precipitation. The cDNAs were ligated to
                     Lone-linker LL-Sal4, purified by phenol/chloroform, and
                     separated from free linkers by Centricon 100. Then, the
                     cDNAs were amplified by long-range high fidelity PCR using
                     Ex Taq polymerase (Takara) with a primer Sal4-S. The
                     products were purified by phenol/chloroform and Centricon
                     100. The cDNAs were digested with SalI and NotI enzymes
                     and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
                     vector. The DH10B E. coli host was transformed with the
                     ligation mixture by the standard chemical method. The
                     average insert size is about 2.5 kb. The library was
                     constructed by Yulan Piao."
ORIGIN

  Query Match             0.5%;  Score 22;  DB 7;  Length 394;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1417 TTTCACATGAACATCCTTCTCC 1438
              ||||||||||||||||||||||
Db         56 TTTCACATGAACATCCTTCTCC 77


RESULT 14
CB807101
LOCUS       CB807101                407 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  AMGNNUC:SRPB2-00129-B10-A srpb2 (10220) Rattus norvegicus cDNA
            clone srpb2-00129-b10 5', mRNA sequence.
ACCESSION   CB807101
VERSION     CB807101.1  GI:29925806
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 407)
  AUTHORS   Amgen EST Program.
  TITLE     Amgen Rat EST Program
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Dan Fitzpatrick
            Amgen, Inc
            One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
            Plate: 00129  row: b  column: 10.
FEATURES             Location/Qualifiers
     source          1. .407
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="srpb2-00129-b10"
                     /tissue_type="prostate tissue"
                     /clone_lib="srpb2 (10220)"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat
                     prostate normalized double selected poly(A+) mRNA size
                     fraction > 1 kb"
ORIGIN

  Query Match             0.5%;  Score 22;  DB 6;  Length 407;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        482 TTGAAAACACTGCTGCTGACTG 503
              ||||||||||||||||||||||
Db        167 TTGAAAACACTGCTGCTGACTG 188


RESULT 15
BE406757
LOCUS       BE406757                425 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  WHE0406_e11_e11zS Wheat etiolated seedling root cDNA library
            Triticum aestivum cDNA clone WHE0406_e11_e11, mRNA sequence.
ACCESSION   BE406757
VERSION     BE406757.1  GI:9366225
KEYWORDS    EST.
SOURCE      Triticum aestivum (bread wheat)
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 425)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D.,
            Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
            Seaton,C.L. and Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes
```

```
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Strategene SK primer.
FEATURES             Location/Qualifiers
     source          1. .425
                     /organism="Triticum aestivum"
                     /mol_type="mRNA"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE0406_e11_e11"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli SOLR"
                     /clone_lib="Wheat etiolated seedling root cDNA library"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Seeds were
                     surface-sterilized, germinated and grown aseptically in
                     the  dark at room temperature on filter paper with water,
                     nystatin and  cefotaxime in covered crystallization
                     dishes. Roots were harvested.  The tissue, total RA, and
                     poly(A) RNA were prepared, a cDNA library  was made, and
                     the cDNA clones were in vivo excised to give pBluescript
                     phagemids in the TJ Close lab (Choi, Close, Fenton) at the
                     University  of California, Riverside.  Plasmid DNA
                     preparations and DNA sequencing  were performed in the OD
                     Anderson lab (all other authors)."
ORIGIN

  Query Match             0.5%;  Score 22;  DB 2;  Length 425;
  Best Local Similarity   100.0%;  Pred. No. 28;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1482 TCTCCAGGACTTCTGTGCCGCC 1503
              ||||||||||||||||||||||
Db        117 TCTCCAGGACTTCTGTGCCGCC 138


Search completed: July 19, 2005, 11:09:20
Job time : 12248 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 18, 2005, 14:43:30 ; Search time 17004 Seconds
(without alignments)
11498.283 Million cell updates/sec

Title: US-10-066-521-5
Perfect score: 4035
Sequence: 1 atggaaggagacaaatcgct.....tcgaggggctggtgtcttaa 4035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match %	Length	DB	ID	Description
	1	3172.6	78.6	3885	9	AY154460	AY154460 Homo sapi
	2	3166.2	78.5	3885	9	AY054986	AY054986 Homo sapi
	3	3166.2	78.5	3900	6	AX427610	AX427610 Sequence
	4	3139	77.8	3830	6	AX704823	AX704823 Sequence
	5	3133.6	77.7	3489	6	AX478549	AX478549 Sequence
	6	3133.6	77.7	3926	6	AX704821	AX704821 Sequence
	7	3057.8	75.8	5859	6	AX459881	AX459881 Sequence
	8	3057.8	75.8	6939	6	AX459873	AX459873 Sequence
	9	3057.8	75.8	6939	6	AX459891	AX459891 Sequence
	10	2553.8	63.3	2753	6	CQ731113	CQ731113 Sequence
c	11	1598.8	39.6	157141	9	AC011470	AC011470 Homo sapi
	12	1598.8	39.6	193609	9	AC024580	AC024580 Homo sapi
	13	1566	38.8	3545	4	AY721594	AY721594 Bos tauru
	14	1287.8	31.9	3405	10	AY329487	AY329487 Mus muscu
	15	1286.2	31.9	3432	10	AY329484	AY329484 Mus muscu
	16	1282.8	31.8	3480	10	AY196361	AY196361 Mus muscu
	17	1281.2	31.8	3470	10	AY196362	AY196362 Mus muscu
	18	1279.6	31.7	3453	10	AY329486	AY329486 Mus muscu
	19	1278	31.7	3447	6	AX427592	AX427592 Sequence
	20	1278	31.7	3447	10	AF074018	AF074018 Mus muscu
	21	1278	31.7	3454	10	AY329490	AY329490 Mus muscu
	22	1276.4	31.6	3534	10	BC053384	BC053384 Mus muscu
	23	1152.8	28.6	1157	6	AX427588	AX427588 Sequence
	24	1144	28.4	3375	10	AY329489	AY329489 Mus muscu
	25	1140.8	28.3	3372	10	AY329485	AY329485 Mus muscu
	26	1008.6	25.0	3303	10	AY329488	AY329488 Mus muscu
	27	1005.4	24.9	3303	10	AY329491	AY329491 Mus muscu
c	28	988.6	24.5	167509	2	AC012107	AC012107 Homo sapi
c	29	840.4	20.8	193662	2	AC127352	AC127352 Mus muscu
c	30	840.4	20.8	213424	2	AC148980	AC148980 Mus muscu
	31	840.4	20.8	299377	2	AC127238	AC127238 Mus muscu
	32	756.6	18.8	1075	6	AX427590	AX427590 Sequence
	33	729.4	18.1	3282	9	AY154469	AY154469 Homo sapi
c	34	649.4	16.1	231371	2	AC132633	AC132633 Rattus no
	35	649.4	16.1	323826	2	AC110429	AC110429 Rattus no
	36	645.2	16.0	1576	10	F143559S07	AF143565 Mus muscu
	37	528.4	13.1	167509	2	AC012107	AC012107 Homo sapi
	38	430.4	10.7	2964	10	AY596199	AY596199 Mus muscu
	39	428.8	10.6	3281	10	AY673647	AY673647 Mus muscu
	40	422.4	10.5	3190	6	AX714395	AX714395 Sequence
	41	422.4	10.5	3190	9	AK056688	AK056688 Homo sapi
	42	422.4	10.5	3333	9	AF442488	AF442488 Homo sapi
	43	422.4	10.5	3339	9	AY072792	AY072792 Homo sapi
	44	422.4	10.5	3368	9	AF479747	AF479747 Homo sapi
	45	419.2	10.4	2575	6	AX320139	AX320139 Sequence

ALIGNMENTS

RESULT 1
AY154460
LOCUS AY154460 3885 bp mRNA linear PRI 20-FEB-2003
DEFINITION Homo sapiens NALP5 (NALP5) mRNA, complete cds.
ACCESSION AY154460
VERSION AY154460.1 GI:28436363
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3885)
AUTHORS Tschopp,J., Martinon,F. and Burns,K.
TITLE NALPs: a novel protein family involved in inflammation
JOURNAL Nat. Rev. Mol. Cell Biol. 4 (2), 95-104 (2003)
MEDLINE 22451042
PUBMED 12563287
REFERENCE 2 (bases 1 to 3885)
AUTHORS Martinon,F., Hofmann,K. and Tschopp,J.
TITLE Direct Submission
JOURNAL Submitted (25-SEP-2002) Institute of Biochemistry, University of Lausanne, ch. des Boveresses 155, Epalinges, VD 1066, Switzerland
FEATURES Location/Qualifiers
source 1. .3885
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
gene 1. .3885
/gene="NALP5"
CDS 1. .3603
/gene="NALP5"
/note="member of the NALP protein family involved in inflammation; contains NACHT, LRR and PYD domains; similar to mouse MATER protein"
/codon_start=1
/product="NALP5"
/protein_id="AAO18156.1"
/db_xref="GI:28436364"
/translation="MKVAGGLELGAAALLSASPRALVTLSTGPTCSILPKNPLFPQNL
SSQPCIKMEGDKSLTPSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIE
NANVECLALLLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKRHSPEDPEATMTD
QGPSKEKVPGISQAVQQDSATAAETKEQEISQAMEQEGATAAETEEQEISQAMEQEGA

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                     TAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWG
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                     FISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIR
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ORIGIN

  Query Match           78.6%;  Score 3172.6;  DB 9;  Length 3885;
  Best Local Similarity  96.3%;  Pred. No. 0;
  Matches 3308;  Conservative    0;  Mismatches    4;  Indels  123;  Gaps    1;

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Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
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Qy        290 ----------------------------------------------------AAATTTCA 297
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Qy        358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
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Qy        418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
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Qy        478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
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Qy        538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
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Qy        658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
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Qy        718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
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Qy        778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
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Qy        838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
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Qy        898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
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Qy       1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
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Db       1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353

Qy       1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
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Qy       1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
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Qy       1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
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Qy       1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
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Qy       1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
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Db       1654 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1713

Qy       1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
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Qy       1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
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Qy       1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
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Qy       1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
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Qy       1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
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Qy       1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
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Qy       1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
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Qy       2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
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Qy       2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
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RESULT 2
AY054986
LOCUS       AY054986               3885 bp    mRNA    linear   PRI 02-APR-2002
DEFINITION  Homo sapiens maternal-antigen-that-embryos-require protein (MATER)
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ACCESSION   AY054986
VERSION     AY054986.1  GI:19882272
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 3885)
  AUTHORS   Tong,Z.B., Bondy,C.A., Zhou,J. and Nelson,L.M.
  TITLE     A human homologue of mouse Mater, a maternal effect gene essential
            for early embryonic development
  JOURNAL   Hum. Reprod. 17 (4), 903-911 (2002)
  MEDLINE   21922687
   PUBMED   11925379
REFERENCE   2  (bases 1 to 3885)
  AUTHORS   Tong,Z.-B., Bondy,C.A. and Nelson,L.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-AUG-2001) Developmental Endocrinology Branch, NICHD,
            NIH, 10 Center Drive, Bethesda, MD 20892/1862, USA
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ORIGIN

  Query Match           78.5%;  Score 3166.2;  DB 9;  Length 3885;
  Best Local Similarity  96.2%;  Pred. No. 0;
  Matches 3304;  Conservative    0;  Mismatches    8;  Indels  123;  Gaps    1;

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Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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VERSION     AX427610.1  GI:21537730
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nelson,L.M. and Tong,Z.-B.
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ORIGIN

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Qy        718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
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Db        994 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 1053

Qy        778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
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Qy        838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
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Qy        898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
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Db       1174 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 1233

Qy        958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
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Qy       1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
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Qy       1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
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Db       1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533

Qy       1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
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Qy       1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
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Qy       1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
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Qy       1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
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Qy       1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
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Db       2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313

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Qy       2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
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Qy       2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
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Qy       2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
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Qy       2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
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Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
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Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
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Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
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Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
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Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
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Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
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Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
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Qy       3178 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3237
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RESULT 4
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DEFINITION  Sequence 3 from Patent EP1285964.
ACCESSION   AX704823
VERSION     AX704823.1  GI:29561488
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Weiss,B., Lessl,M., Peters-Kottig,M. and Beckmann,G.
  TITLE     Human mater proteins
  JOURNAL   Patent: EP 1285964-A 3 26-FEB-2003;
            SCHERING AKTIENGESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
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ORIGIN

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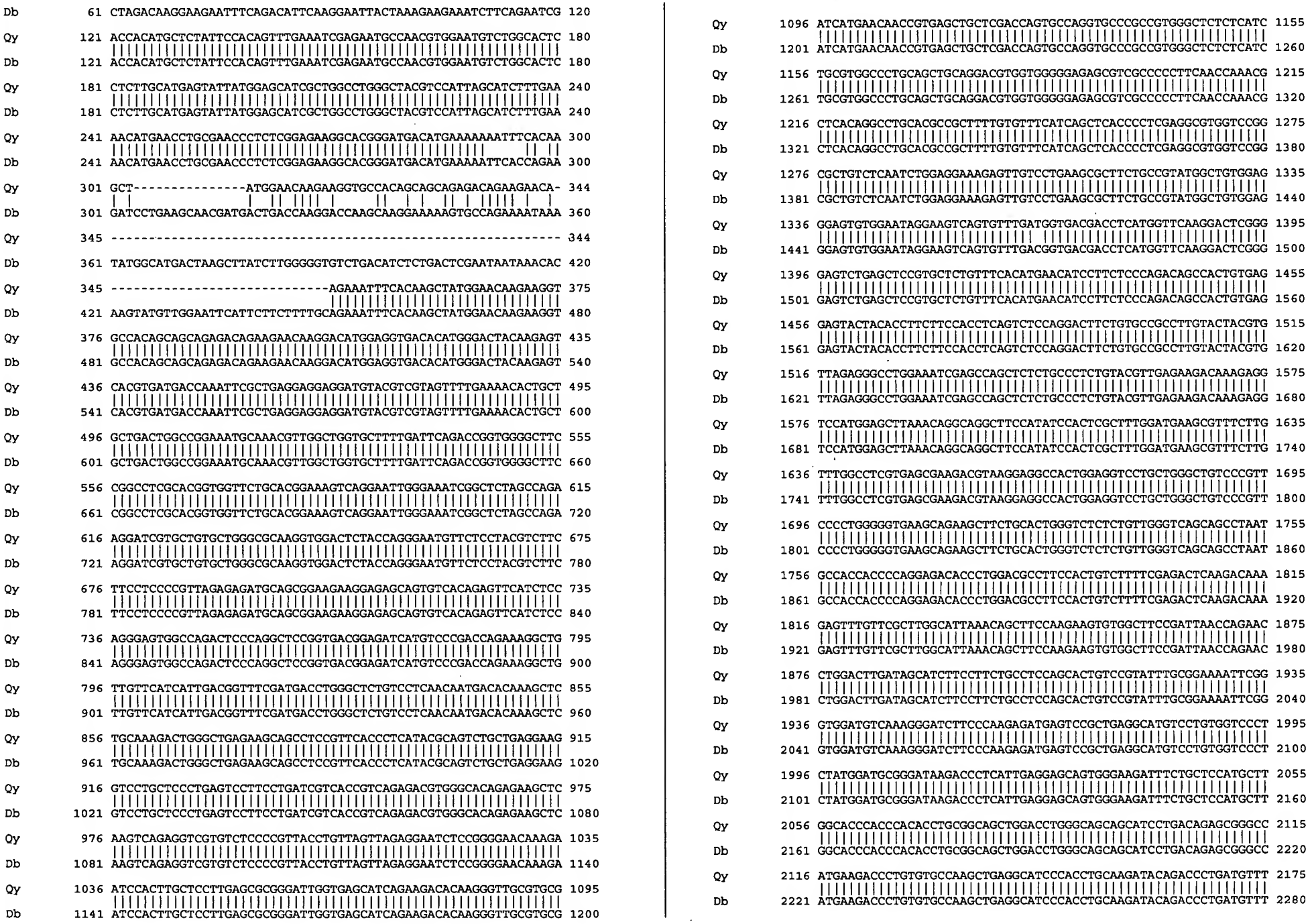

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Qy       2236 AACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCG 2295
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Db       2341 AACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCG 2400

Qy       2296 TGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGA 2355
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Qy       2896 TCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTG 2955
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Qy       2956 GGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACG 3015
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Db       3061 GGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACG 3120

Qy       3016 AGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCC 3075
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Qy       3076 CTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAA 3135
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Qy       3136 GGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGG 3195
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Qy       3196 CTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTC 3255
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Qy       3256 AAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
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RESULT 5
AX478549
LOCUS       AX478549               3489 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 3 from Patent WO0248362.
ACCESSION   AX478549
VERSION     AX478549.1  GI:22217318
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE   1
  AUTHORS   Ramkumar,J. and Arvizu,C.
  TITLE     Embryogenesis associated proteins
  JOURNAL   Patent: WO 0248362-A 3 20-JUN-2002;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match            77.7%;  Score 3133.6;  DB 6;  Length 3489;
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  Matches 3308;  Conservative    0;  Mismatches    4;  Indels  162;  Gaps    1;

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Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
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Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
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Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300

Qy        290 ---------------------------------------------------------- 289

Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

Qy        290 ---------------------------------------------------------- 289

Db        361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420

Qy        290 ------------------------------AAATTTCACAAGCTATGGAACAAGAAGGT 318
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RESULT 6
AX704821
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DEFINITION  Sequence 1 from Patent EP1285964.
ACCESSION   AX704821
VERSION     AX704821.1  GI:29561487
KEYWORDS    .
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Weiss,B., Lessl,M., Peters-Kottig,M. and Beckmann,G.
  TITLE     Human mater proteins
  JOURNAL   Patent: EP 1285964-A 1 26-FEB-2003;
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ORIGIN

  Query Match           77.7%;  Score 3133.6;  DB 6;  Length 3926;
  Best Local Similarity  95.2%;  Pred. No. 0;
  Matches 3308;  Conservative    0;  Mismatches    4;  Indels  162;  Gaps    1;
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Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
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Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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Qy        290 ---------------------------------------------------------- 289

Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

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Qy      2359 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2418
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Qy      2419 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2478
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Qy      2539 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2598
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Db      2821 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2880
Qy      2719 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2778
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Qy      2779 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 2838
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Qy      3079 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3138
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Qy       3139 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3198
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Db       3301 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3360

Qy       3199 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3258
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Db       3361 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3420

Qy       3259 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
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RESULT 7
AX459881
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DEFINITION  Sequence 24 from Patent WO0240668.
ACCESSION   AX459881
VERSION     AX459881.1  GI:21725649
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tschopp,J. and Martinon,F.
  TITLE     Proteins and dna sequences underlying these proteins used for
            treating inflammations
  JOURNAL   Patent: WO 0240668-A 24 23-MAY-2002;
            Apotech Research and Development Ltd. (CH)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 3192;  Conservative    0;  Mismatches    2;  Indels  123;  Gaps    1;

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Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
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Db       2095 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 2154

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
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Db       2155 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 2214

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
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Db       2215 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 2274

Qy        290 ---------------------------------------------------------- 289

Db       2275 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 2334

Qy        290 ----------------------------------------------------------AAATTTCA 297
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Db       2335 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAAGAAATTTCA 2394

Qy        298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
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Db       2395 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 2454

Qy        358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
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Qy        538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
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Qy        598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
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Db       2695 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 2754

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Qy        718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
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Db       2815 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 2874

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Db       2875 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 2934

Qy        838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
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Db       2935 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 2994

Qy        898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
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Db       2995 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 3054

Qy        958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
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Db       3055 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 3114

Qy       1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
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Db       3115 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 3174

Qy       1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
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Db       3175 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 3234

Qy       1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
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Db       3235 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 3294

Qy       1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3295 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 3354

Qy       1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
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Qy       1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
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Db       3415 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTC 3474

Qy       1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
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Db       3475 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 3534
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Qy       1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
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Db       3535 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 3594

Qy       1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
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Db       3595 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 3654

Qy       1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
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Qy       1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
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Qy       1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
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Qy       1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
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Qy       1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
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Qy       1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
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Qy       2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
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Qy       2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
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Qy       2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
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Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
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Db       4855 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 4914

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Db       4915 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 4974

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Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
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Db       5215 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 5274

Qy       3178 AACTTACAGATAATTGG 3194
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RESULT 8
AX459873
LOCUS       AX459873               6939 bp    DNA     linear   PAT 30-NOV-2002
DEFINITION  Sequence 16 from Patent WO0240668.
ACCESSION   AX459873
VERSION     AX459873.1  GI:21725645
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tschopp,J. and Martinon,F.
  TITLE     Proteins and dna sequences underlying these proteins used for
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  JOURNAL   Patent: WO 0240668-A 16 23-MAY-2002;
            Apotech Research and Development Ltd. (CH)
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ORIGIN
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Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
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Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
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Qy        290 ---------------------------------------------------------- 289

Db       3355 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 3414

Qy        290 ----------------------------------------------------AAATTTCA 297
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Qy        478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
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Qy        538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3775 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 3834

Qy        658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
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Qy        718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
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Db       4015 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 4074

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RESULT 9
AX459891
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DEFINITION  Sequence 34 from Patent WO0240668.
ACCESSION   AX459891
VERSION     AX459891.1  GI:21725654
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tschopp,J. and Martinon,F.
  TITLE     Proteins and dna sequences underlying these proteins used for
            treating inflammations
  JOURNAL   Patent: WO 0240668-A 34 23-MAY-2002;
            Apotech Research and Development Ltd. (CH)
FEATURES             Location/Qualifiers
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                     /note="NALP13/Py17.cdna"
ORIGIN

  Query Match           75.8%;  Score 3057.8;  DB 6;  Length 6939;
  Best Local Similarity   96.2%;  Pred. No. 0;
  Matches 3192;  Conservative    0;  Mismatches    2;  Indels  123;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
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Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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Qy       958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
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Qy      1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
Db      4915 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 4974
Qy      1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
Db      4975 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 5034
Qy      1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
Db      5035 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 5094
Qy      1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
Db      5095 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 5154
Qy      1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
Db      5155 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 5214
Qy      2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
Db      5215 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 5274
Qy      2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
Db      5275 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 5334
Qy      2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
Db      5335 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 5394
Qy      2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
Db      5395 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 5454
Qy      2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
Db      5455 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 5514
Qy      2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
Db      5515 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 5574
Qy      2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457
Db      5575 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 5634
Qy      2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517
Db      5635 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 5694
Qy      2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
Db      5695 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 5754
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Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
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Db       5755 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 5814

Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
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Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
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Db       5875 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 5934

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
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Db       5935 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 5994

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
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Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
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Db       6055 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 6114

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
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Db       6115 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAA 6174

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
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Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
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Db       6235 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 6294

Qy       3118 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3177
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Db       6295 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 6354

Qy       3178 AACTTACAGATAATTGG 3194
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RESULT 10
CQ731113
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DEFINITION  Sequence 17047 from Patent WO02068579.
ACCESSION   CQ731113
VERSION     CQ731113.1  GI:42306827
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 17047 06-SEP-2002;
            PE Corporation (NY) (US)
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ORIGIN

  Query Match           63.3%;  Score 2553.8;  DB 6;  Length 2753;
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGG 60

Qy        464 AGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGG 523
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGG 120

Qy        524 CTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAA 583
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        584 AGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTG 643
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTG 240

Qy        644 GACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGA 703
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGA 300

Qy        704 AGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGG 763
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Db        301 AGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGG 360

Qy        764 TGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACC 823
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Db        361 TGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACC 420

Qy        824 TGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTC 883
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Db        421 TGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTC 480

Qy        884 CGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCG 943
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Qy        944 TCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACC 1003
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Db        541 TCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACC 600

Qy       1004 TGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTG 1063
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Db        601 TGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTG 660

Qy       1064 GTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACC 1123
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Db        661 GTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACC 720

Qy       1124 AGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGG 1183
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Db        721 AGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGG 780

Qy       1184 TGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGT 1243
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Db        781 TGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGT 840

Qy       1244 TTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTG 1303
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Db        841 TTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTG 900

Qy       1304 TCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTG 1363
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Db        901 TCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTG 960

Qy       1364 ATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACA 1423
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Db        961 ATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACA 1020

Qy       1424 TGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTC 1483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1484 TCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTC 1543
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Qy       1544 TCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCC 1603
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Qy       1604 ATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGA 1663
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Db       1201 ATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGA 1260

Qy       1664 GGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGC 1723
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Db       1261 GGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGC 1320

Qy       1724 ACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACG 1783
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Db       1321 ACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACG 1380

Qy       1784 CCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCT 1843
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Db       1381 CCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCT 1440

Qy       1844 TCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCC 1903
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Db       1441 TCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCC 1500

Qy       1904 TCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAG 1963
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Db       1501 TCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAG 1560

Qy       1964 ATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTG 2023
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Db       1561 ATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTG 1620

Qy       2024 AGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGG 2083
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Qy       2084 ACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGC 2143
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Qy       2144 ATCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGC 2203
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Qy       2204 AGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCA 2263
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Qy       2264 CCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTT 2323
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Qy       2324 TGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCT 2383
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Db       1921 TGTTGGAGTCTTTGAG---------------------------------------------- 1936

Qy       2384 CCCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGA 2443

Db       1937 ---------------------------------------------------------- 1936

Qy       2444 CAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGA 2503

Db       1937 ---------------------------------------------------------- 1936

Qy       2504 AGCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCC 2563
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Qy       2564 TCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAG 2623
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Qy       2624 GTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGC 2683
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Qy       2684 TGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTA 2743
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Db       2110 TGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTA 2169

Qy       2744 ACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGC 2803
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Db       2170 ACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGC 2229

Qy       2804 TTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGT 2863
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Qy       3044 CTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTC 3103
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Qy       3104 TAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTG 3163
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Qy       3164 CCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAA 3223
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Qy       3224 TAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTT 3283
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Qy       3284 GGCATTCTTTTGATGAAGATGACCGACAC 3312
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RESULT 11
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LOCUS       AC011470              157141 bp    DNA     linear   PRI 15-JUL-2000
DEFINITION  Homo sapiens chromosome 19 clone CTC-490M10, complete sequence.
ACCESSION   AC011470
VERSION     AC011470.5  GI:9211204
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 157141)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 157141)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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REFERENCE   3  (bases 1 to 157141)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jul 15, 2000 this sequence version replaced gi:7690109.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.9% of Sequence;
            Estimated Total Number of Errors is 0.1.
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ORIGIN

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  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        400 CAAGGACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAG 459
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      42003 CCAGGACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAG 41944

Qy        460 GAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACG 519
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41943 GAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACG 41884

Qy        520 TTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCAC 579
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      41883 TTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCAC 41824

Qy        580 GGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAA 639
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Db      41823 GGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAA 41764

Qy        640 GGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAG 699
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Db      41763 GGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAG 41704

Qy        700 CGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCT 759
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Db      41703 CGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCT 41644

Qy        760 CCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGAT 819
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Db      41643 CCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGAT 41584

Qy        820 GACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAG 879
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Db      41583 GACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAG 41524

Qy        880 CCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTG 939
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Qy        940 ATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGT 999
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Qy       1000 TACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGG 1059
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Qy       1060 ATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTC 1119
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Qy       1120 GACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGAC 1179
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Db      41283 GACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGAC 41224

Qy       1180 GTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTT 1239
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Db      41223 GTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTT 41164

Qy       1240 GTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGA 1299
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Db      41163 GTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGA 41104

Qy       1300 GTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTG 1359
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Qy       1360 TTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTT 1419
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Qy       1420 CACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTC 1479
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Qy       1480 AGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCA 1539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1540 GCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGC 1599
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Db      40863 GCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGC 40804

Qy       1600 TTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTA 1659
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Db      40803 TTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTA 40744

Qy       1660 AGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTT 1719
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Db      40743 AGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTT 40684

Qy       1720 CTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTG 1779
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Db      40683 CTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTG 40624

Qy       1780 GACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAAC 1839
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Db      40623 GACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAAC 40564

Qy       1840 AGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTC 1899
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Db      40563 AGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTC 40504

Qy       1900 TGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCA 1959
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Db      40503 TGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCA 40444

Qy       1960 AGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGG 2001
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Db      40443 AGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGG 40402


RESULT 12
AC024580
LOCUS       AC024580              193609 bp    DNA     linear   PRI 21-DEC-2001
DEFINITION  Homo sapiens chromosome 19 clone CTD-2621I17, complete sequence.
ACCESSION   AC024580
VERSION     AC024580.6  GI:17975240
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 193609)
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  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 193609)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 193609)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-NOV-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 193609)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Dec 21, 2001 this sequence version replaced gi:16905144.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 99.4% of Sequence;
            Estimated Total Number of Errors is 0.9.
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  Query Match             39.6%;  Score 1598.8;  DB 9;  Length 193609;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1600;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        400 CAAGGACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAG 459
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22255 CCAGGACATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAG 22314

Qy        460 GAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACG 519
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Db      22315 GAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACG 22374

Qy        520 TTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCAC 579
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Db      22375 TTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCAC 22434

Qy        580 GGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAA 639
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Db      22435 GGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAA 22494

Qy        640 GGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAG 699
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Db      22495 GGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAG 22554

Qy        700 CGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCT 759
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Db      22555 CGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCT 22614

Qy        760 CCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGAT 819
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      22615 CCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGAT 22674

Qy        820 GACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAG 879
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Db      22675 GACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAG 22734

Qy        880 CCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTG 939
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Db      22735 CCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTG 22794

Qy        940 ATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGT 999
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Db      22795 ATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGT 22854

Qy       1000 TACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGG 1059
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Db      22855 TACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGG 22914

Qy       1060 ATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTC 1119
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Db      22915 ATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTC 22974

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Db      22975 GACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGAC 23034

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Db      23095 GTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGA 23154

Qy       1300 GTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTG 1359
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Qy       1360 TTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTT 1419
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Db      23215 TTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTT 23274

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Qy       1480 AGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCA 1539
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Db      23395 GCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGC 23454

Qy       1600 TTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTA 1659
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Qy       1660 AGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTT 1719
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Qy       1840 AGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTC 1899
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Db      23695 AGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTC 23754

Qy       1900 TGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCA 1959
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Db      23755 TGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCA 23814

Qy       1960 AGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGG 2001
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Db      23815 AGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGG 23856
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RESULT 13
AY721594
LOCUS       AY721594               3545 bp    mRNA    linear   MAM 15-SEP-2004
DEFINITION  Bos taurus maternal antigen that embryo require mRNA, complete cds.
ACCESSION   AY721594
VERSION     AY721594.1  GI:51980124
KEYWORDS    .
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 3545)
  AUTHORS   Pennetier,S., Uzbekova,S., Perreau,C., Papillier,P., Mermillod,P.
            and Dalbies-Tran,R.
  TITLE     Spatio-Temporal Expression of the Germ Cell Marker Genes MATER,
            ZAR1, GDF9, BMP15, and VASA in Adult Bovine Tissues, Oocytes, and
            Preimplantation Embryos
  JOURNAL   Biol. Reprod. (2004) In press
REFERENCE   2  (bases 1 to 3545)
  AUTHORS   Pennetier,S., Uzbekova,S. and Dalbies-Tran,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-2004) Physiologie de la Reproduction et des
            Comportements, Institut National de la Recherche Agronomique,
            Nouzilly 37380, France
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ORIGIN

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  Matches 2271;  Conservative    0;  Mismatches 1005;  Indels   42;  Gaps    6;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              |||  || || ||||     | |||| ||||  ||||| ||||| |||||| || |  ||
Db          1 ATGAGAGAAGCCAAAATAGCCCCCTTATCCAATTACGGACTGCAGTGGTGTTTCGAGCAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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Db         61 CTGGGCAAAGAGGAGTTCCAGACATTTAAGGCCCTCCTGAAGGAGCATGCGTCAGAATCA 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
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Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
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Qy        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420
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Qy        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480
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Qy        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540
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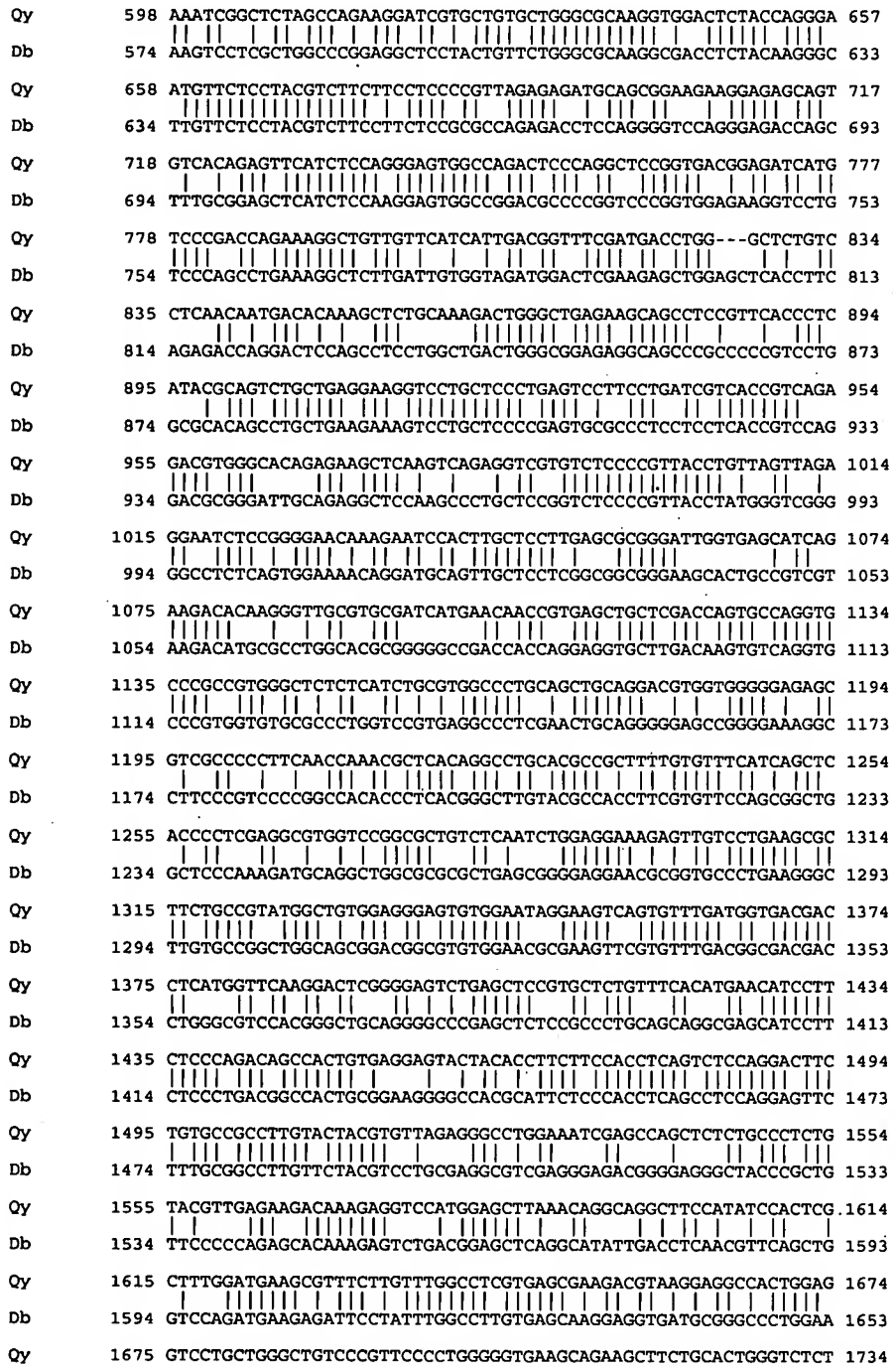
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Qy       2875 GCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTG 2934
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Qy       3295 GATGAAGATGACCGACAC 3312
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RESULT 14
AY329487
LOCUS       AY329487               3405 bp    mRNA    linear   ROD 18-DEC-2003
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ACCESSION   AY329487
VERSION     AY329487.1  GI:37595472
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SOURCE      Mus musculus (house mouse)
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3405)
  AUTHORS   Cheng,H., Zhang,Y., Huang,Z. and Ma,R.Z.
  TITLE     Identification and characterization of alternative splice variants
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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3405)
  AUTHORS   Cheng,H., Huang,Z., Zhang,Y., Liu,H., Teuscher,C. and Ma,R.Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-2003) Human and Animal Genetics Division,
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ORIGIN

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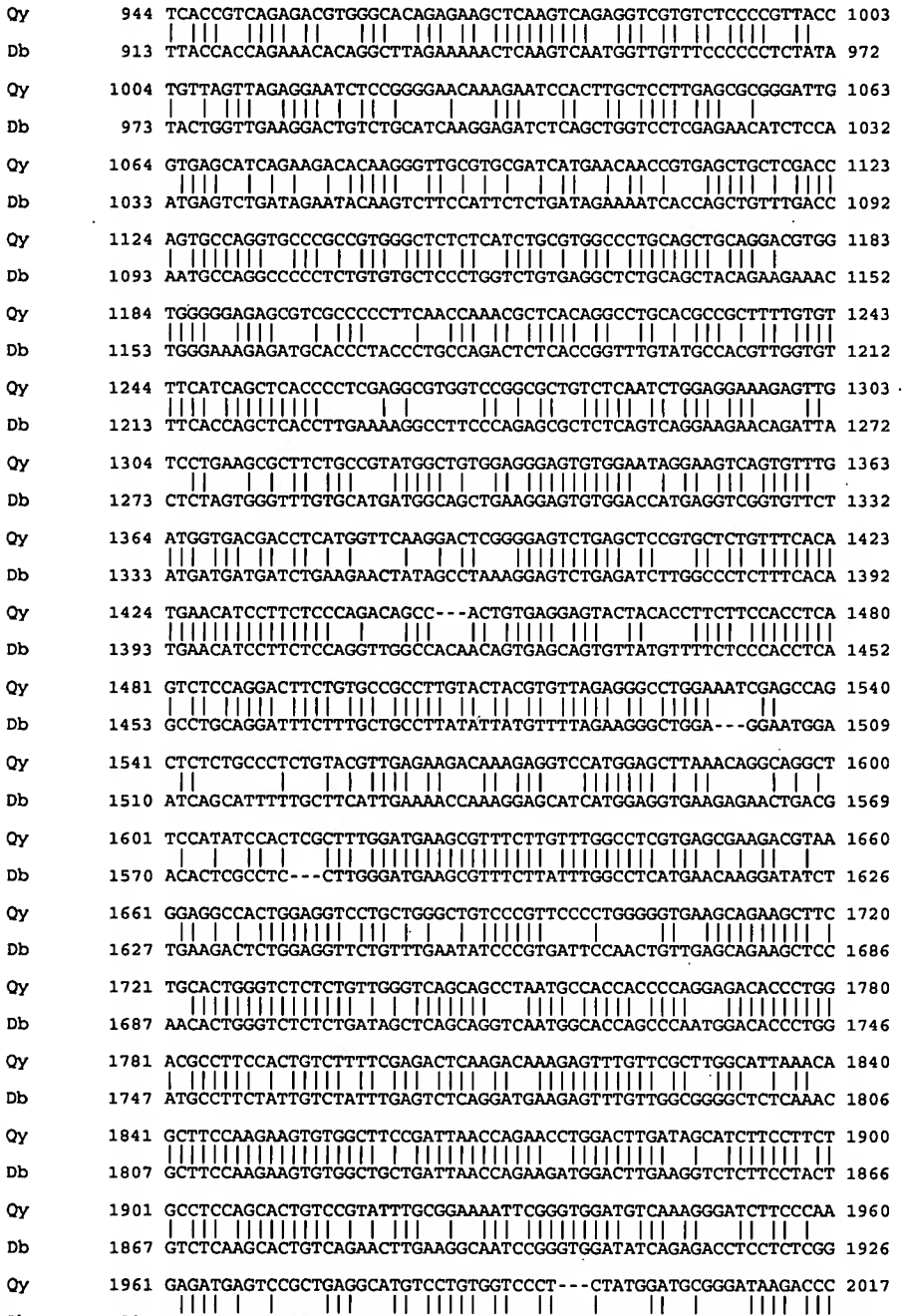
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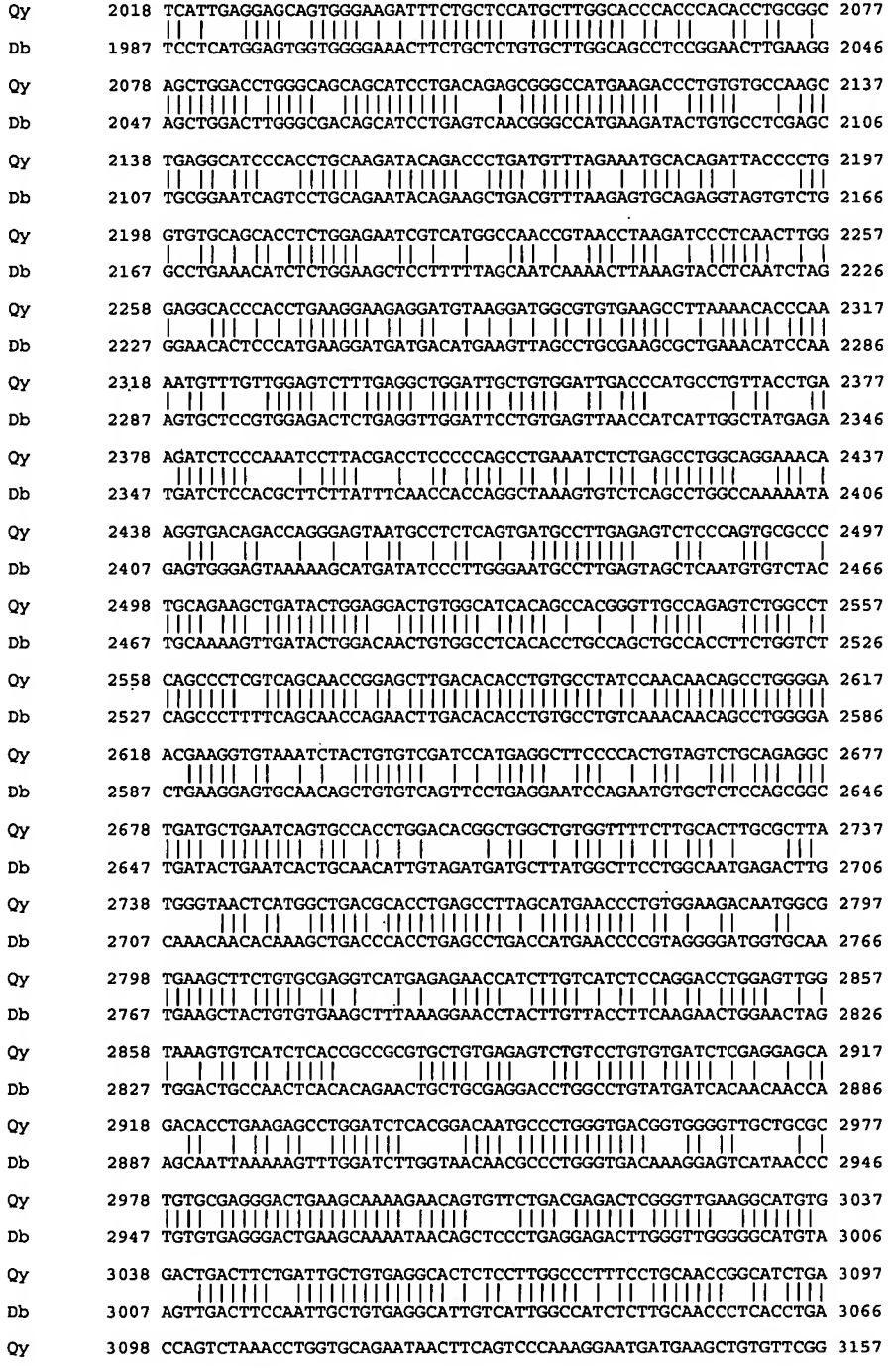
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Db       3187 CCCGAGTGAGAAGACAGCTGGAGGAAGTTGAGTTTGTCAAGCCCCACGTGGTGATTGATG 3246

Qy       3278 GTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312

Db       3247 GTGATTGGTATGCTAGTGATGAAGATGACCGAAAC 3281


RESULT 15
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DEFINITION  Mus musculus strain SWR/J MATER protein isoform-E (Mater) mRNA,
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ACCESSION   AY329484
VERSION     AY329484.1  GI:37595466
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3432)
  AUTHORS   Cheng,H., Zhang,Y., Huang,Z. and Ma,R.Z.
  TITLE     Identification and characterization of alternative splice variants
            for murine Mater
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3432)
  AUTHORS   Cheng,H., Huang,Z., Zhang,Y., Liu,H., Teuscher,C. and Ma,R.Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-2003) Human and Animal Genetics Division,
            Institute of Genetics and Developmental Biology, Chinese Academy of
            Sciences, Building 917, Datun Road, Beijing 100101, P.R.China
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ORIGIN

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Qy        527 GTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGT 586

Db        496 ATGCTTTTAAACCATACCAGAAAACCTTCCAGCCTCACACCATTATCCTACATGGAAGAC 555

Qy        587 CAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGAC 646

Db        556 CAGGAGTTGGGAAGTCAGCTTTGGCCAGAAGTATTGTTCTTGGCTGGGCACAGGGTAAAC 615

Qy        647 TCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGA 706

Db        616 TCTTCCAAAAAATG---TCCTTTGTCATCTTCTTCTCTGTTAGAGAAATAAAGTGGACAG 672

Qy        707 AGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGA 766

Db        673 AGAAGAGCAGTTTGGCACAGCTGATTGCTAAGGAGTGTCCAGACTCCTGGGATCTAGTGA 732

Qy        767 CGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGG 826

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Qy        827 GCTCTGTCCTC---AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTC 883

Db        793 ACTCTGTCCTCCAACATGATGATATGACACTATCCAGAGACTGGAAGGATGAACAGCCCA 852

Qy        884 CGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCG 943

Db        853 TATACATCCTGATGTACAGCCTCCTGAGGAAGGCTCTCCTACCTCAGTCCTTTCTCATCA 912

Qy        944 TCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACC 1003

Db        913 TTACCACCAGAAACACAGGCTTAGAAAAACTCAAGTCAATGGTTGTGTCCCCCCTCTATA 972

Qy       1004 TGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTG 1063

Db        973 TACTGGTTGAAGGACTGTCTGCATCAAGGAGATCTCAGCTGGTCCTCGAGAACATCTCCA 1032

Qy       1064 GTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACC 1123

Db       1033 ATGAGTCTGATAGAATACAAGTCTTCCATTCTCTGATAGAAAATCACCAGCTGTTTGACC 1092

Qy       1124 AGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGG 1183

Db       1093 AATGCCAGGCCCCCTCTGTGTGCTCCCTGGTCTGTGAGGCTCTGCAGCTACAGAAGAAAC 1152

Qy       1184 TGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGT 1243

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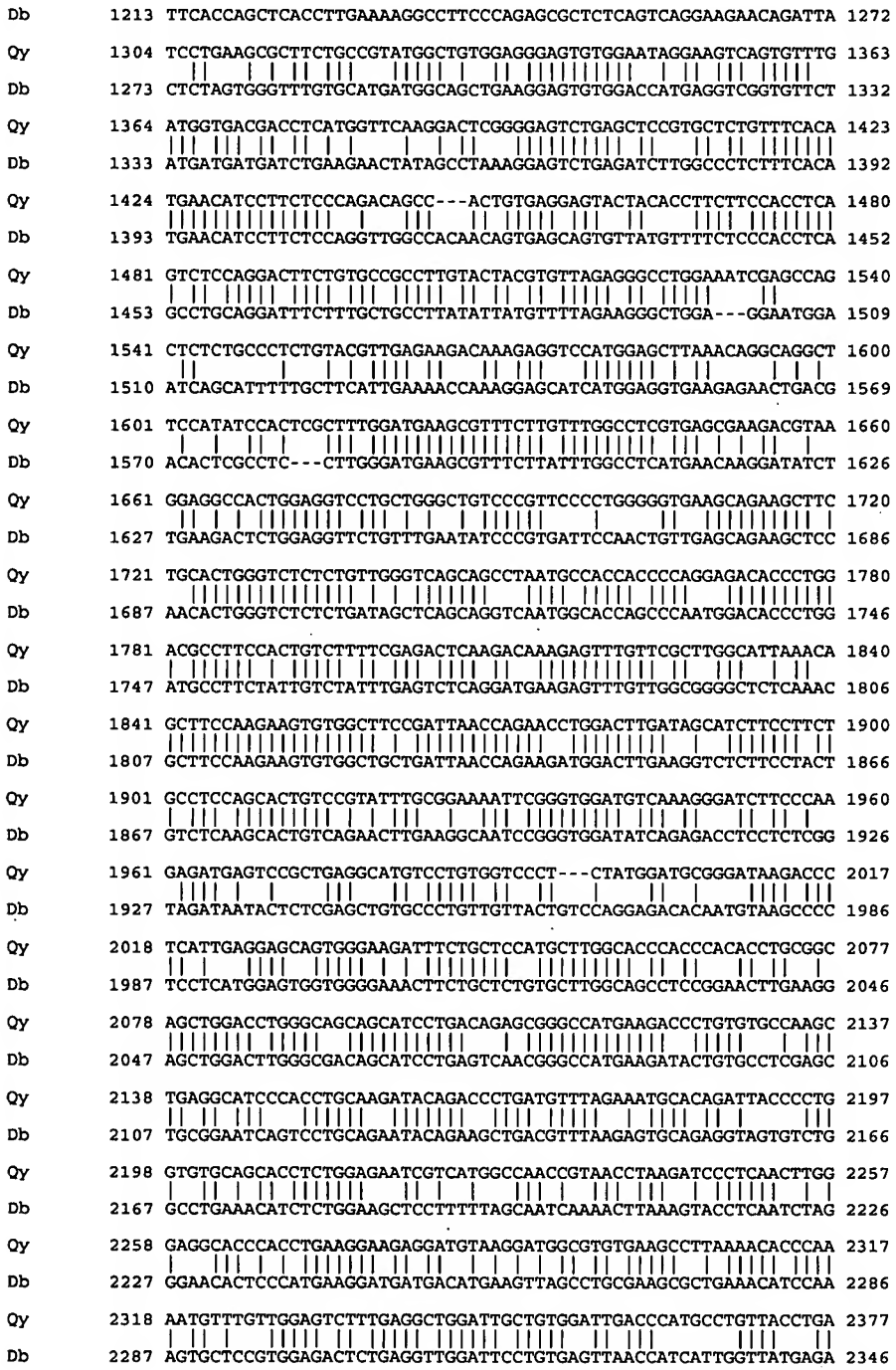

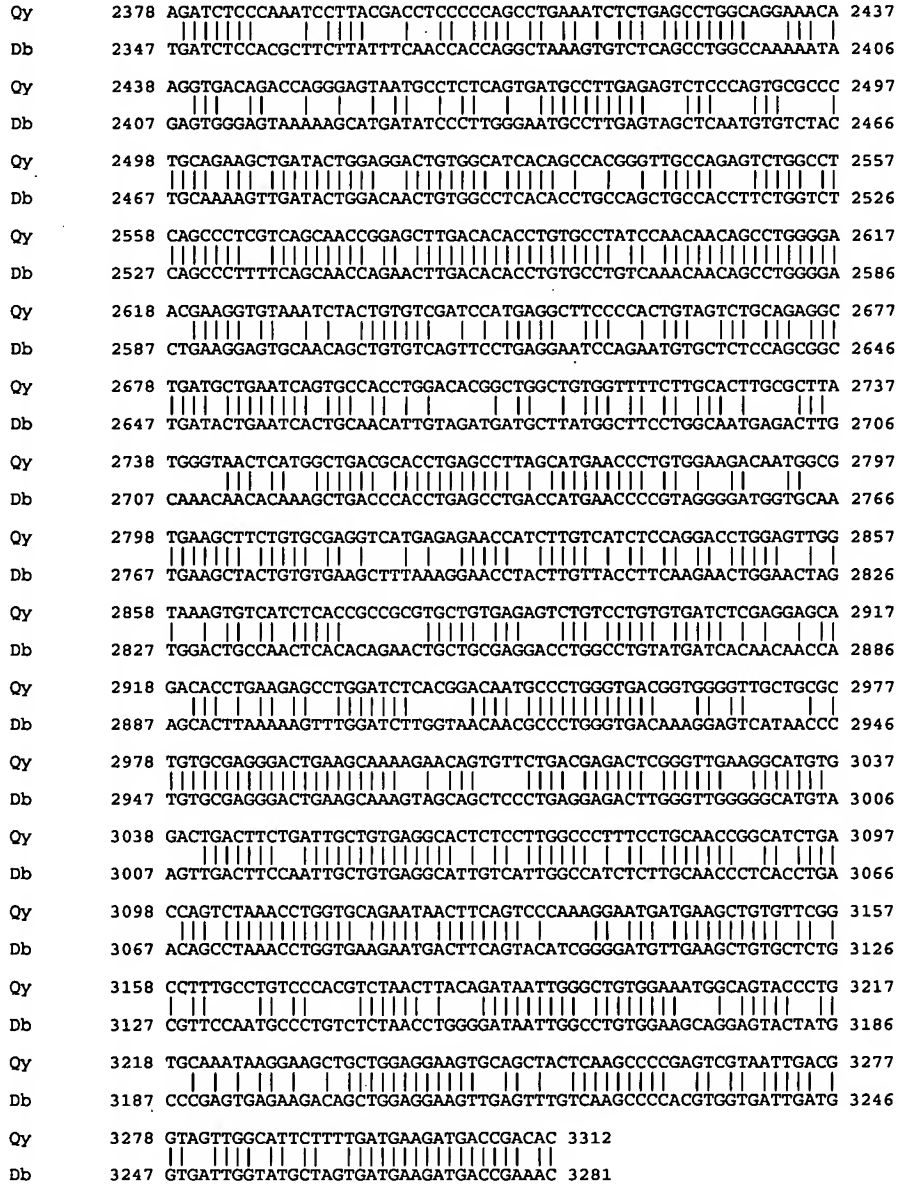

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Job time : 17042 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 18, 2005, 12:25:31 ; Search time 2009 Seconds
(without alignments)
11889.575 Million cell updates/sec

Title: US-10-066-521-5
Perfect score: 4035
Sequence: 1 atggaaggagacaaatcgct.....tcgaggggctggtgtcttaa 4035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: geneseqn2002bs:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4035	100.0	4035	6	AAL44356	Aal44356 Human PYR
2	4035	100.0	4035	10	ADP94744	Adf94744 Human PYR
3	3166.2	78.5	3900	6	ABK48628	Abk48628 Human MAT
4	3166.2	78.5	3900	8	AAD49018	Aad49018 Human MAT
5	3139	77.8	3830	8	ADA45220	Ada45220 Human MAT
6	3133.6	77.7	3489	6	AAD41224	Aad41224 Human EMB
7	3133.6	77.7	3926	8	ADA45218	Ada45218 Human MAT
8	3057.8	75.8	5859	6	AAL47135	Aal47135 Pyrin dom
9	3057.8	75.8	6939	6	AAL47131	Aal47131 Pyrin dom
10	3057.8	75.8	6939	6	AAL47140	Aal47140 Pyrin dom
11	2900.6	71.9	3226	6	ABX97181	Abx97181 Human NOV
12	1840.6	45.6	2820	12	ADN62078	Adn62078 Human cDN
13	1278	31.7	3447	6	ABK48611	Abk48611 Mouse MAT
14	1278	31.7	3447	8	AAD49001	Aad49001 Mouse MAT
15	1152.8	28.6	1157	6	ABK48609	Abk48609 Human MAT
16	1152.8	28.6	1157	8	AAD48999	Aad48999 Human MAT
17	756.6	18.8	1075	6	ABK48610	Abk48610 Human MAT
18	756.6	18.8	1075	8	AAD49000	Aad49000 Human MAT
19	536	13.3	2808	12	ADP47735	Adp47735 Human inf
20	527.8	13.1	3039	12	ADP47733	Adp47733 Human inf
21	440	10.9	2775	12	ADO50889	Ado50889 Human NOV
22	438	10.9	2775	10	ADF44704	Adf44704 Human NOV
23	424	10.5	2985	6	ADE36408	Ade36408 Human PAA
24	424	10.5	2985	12	ADJ19330	Adj19330 Human PAN
25	422.4	10.5	2982	10	ADF94764	Adf94764 Human PYR
26	422.4	10.5	3190	10	ADA53511	Ada53511 Human cod
27	422.4	10.5	3368	6	AAL44366	Aal44366 Human PYR
28	422.4	10.5	3368	10	ADF94760	Adf94760 Human PYR
29	419.2	10.4	2575	6	AAI70683	Aai70683 Human nuc
30	419.2	10.4	2767	8	ABT16018	Abt16018 NOVX rela
31	419.2	10.4	3172	6	ABN99366	Abn99366 Human sec
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33	418.8	10.4	2883	12	ADO41637	Ado41637 Novel hum
34	409	10.1	3186	6	AAL44363	Aal44363 Human PYR
35	409	10.1	3186	10	ADF94754	Adf94754 Human PYR
36	404.4	10.0	3108	6	ADE36416	Ade36416 Human PAA
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43	392.6	9.7	3189	5	AAI67185	Aai67185 Nucleotid
44	392.6	9.7	4944	10	ADF14464	Adf14464 Human end
45	381.4	9.5	3431	4	AAD14322	Aad14322 Human nuc

ALIGNMENTS

RESULT 1
AAL44356
ID AAL44356 standard; cDNA; 4035 BP.
XX
AC AAL44356;
XX
DT 31-OCT-2002 (first entry)
XX
DE Human PYRIN-5 cDNA sequence.
XX
KW Human; gene; ss; gene therapy; PYRIN; stress-related response;
KW apoptopic response; inflammatory response; inflammatory disorder;
KW immune system disorder; Crohn's disease; multiple sclerosis; cancer;
KW leukaemia; autoimmune disorder; arthritis; neurological disease;
KW Alzheimer's disease; Parkinson's disease; chromosomal mapping;
KW tissue typing; forensic biology; predictive medicine; pharmacogenomics;
KW transcription profiling; PYRIN-5.
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OS Homo sapiens.
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FH Key Location/Qualifiers
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PN WO200261049-A2.
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PD 08-AUG-2002.
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PF 31-JAN-2002; 2002WO-US002967.
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PR 31-JAN-2001; 2001US-0265231P.
PR 10-SEP-2001; 2001US-0318645P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
PA (AMHP) WYETH.
XX
PI Bertin J, Wang W, Blatcher M;
XX
DR WPI; 2002-627477/67.
DR P-PSDB; AAO15585.
XX
PT New PYRIN polypeptides and nucleic acids useful for modulating and

PT diagnosing stress-related, apoptopic and inflammatory responses, or for
PT treating inflammatory and immune system disorders, cancers, or
PT neurological diseases.
XX
PS Claim 4; Fig 3; 167pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human
CC PYRIN proteins. The PYRIN protein and DNA sequences of the invention are
CC useful for modulating and diagnosing stress-related, apoptopic and
CC inflammatory responses. The PYRIN protein and DNA sequences are useful
CC for treating: inflammatory disorders and immune system disorders (e.g.
CC Crohn's disease, reactive arthritis, multiple sclerosis, contact
CC dermatitis, psoriasis, graft rejection, allergies, viral infections and
CC bacterial infections); cancer (e.g. leukaemia); autoimmune disorders
CC (e.g. systemic lupus erythematosus and arthritis); and neurological
CC diseases (e.g. Alzheimer's disease and Parkinson's disease). The PYRIN
CC protein and DNA sequences may also be used in screening assays, detection
CC assays (e.g. chromosomal mapping, tissue typing or forensic biology),
CC predictive medicine (e.g. diagnostic assays, clinical trials and
CC pharmacogenomics) and transcription profiling. The present DNA sequence
CC encodes the human PYRIN-5 protein
XX
SQ Sequence 4035 BP; 935 A; 1022 C; 1175 G; 903 T; 0 U; 0 Other;

Query Match 100.0%; Score 4035; DB 6; Length 4035;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
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Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
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Qy        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360
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Qy        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420
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Qy        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480
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Db        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480

Qy        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540
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Qy        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600
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Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

Qy        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140

Qy       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200

Qy       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260

Qy       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320

Qy       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380

Qy       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440

Qy       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500

Qy       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560

Qy       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620

Qy       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680

Qy       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740

Qy       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800
Qy       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860
Db       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860
Qy       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
Db       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
Qy       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
Db       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
Qy       1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
Db       1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
Qy       2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Db       2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Qy       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Db       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Qy       2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
Db       2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
Qy       2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
Db       2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
Qy       2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
Db       2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
Qy       2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
Db       2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
Qy       2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
Db       2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
Qy       2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520
Db       2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520
Qy       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
Db       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
Qy       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Db       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Qy       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Db       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Qy       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Db       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Qy       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
Db       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
Qy       2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880
Db       2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880

Qy       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
Db       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
Qy       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
Db       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
Qy       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Db       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Qy       3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
Db       3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
Qy       3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
Db       3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
Qy       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
Db       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
Qy       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
Db       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
Qy       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
Db       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
Qy       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
Db       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
Qy       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Db       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Qy       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
Db       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
Qy       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
Db       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
Qy       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
Db       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
Qy       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
Db       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
Qy       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
Db       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
Qy       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
Db       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
Qy       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
Db       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
Qy       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
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Qy       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020

Qy       4021 GGGCTGGTGTCTTAA 4035
              |||||||||||||||
Db       4021 GGGCTGGTGTCTTAA 4035


RESULT 2
ADF94744
ID   ADF94744 standard; cDNA; 4035 BP.
XX
AC   ADF94744;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Human PYRIN-5 coding sequence.
XX
KW   human; PYRIN; inflammatory disorder; inappropriate apoptosis;
KW   inflammatory bowel disease; rheumatoid arthritis; diabetes;
KW   multiple sclerosis; Grave's disease; contact dermatitis; psoriasis;
KW   graft rejection; asthma; allergy; chronic obstructive pulmonary disease;
KW   glomerulonephritis; infection; Alzheimer's disease; Parkinson's disease;
KW   anaemia; ischaemia; screening; chromosomal mapping; tissue typing;
KW   forensic biology; pharmacogenomics; predictive medicine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003089588-A2.
XX
PD   30-OCT-2003.
XX
PF   14-APR-2003; 2003WO-US011572.
XX
PR   17-APR-2002; 2002US-00124498.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
PA   (AMHP ) WYETH.
XX
PI   Bertin J,  Wang W,  Blatcher M;
XX
DR   WPI; 2003-845527/78.
DR   P-PSDB; ADF94745.
XX
PT   New nucleic acid molecules and polypeptides (e.g. PYRIN-2 or PYRIN-3)
PT   useful for diagnosing, preventing or treating inflammation or disorders
PT   associated with inappropriate apoptosis, in chromosomal mapping or in
PT   pharmacogenomics.
XX
PS   Claim 4; SEQ ID NO 5; 199pp; English.
XX
CC   The invention comprises the amino acid and coding sequences of human
CC   PYRIN proteins. The DNA and protein sequences of the invention are useful
CC   in diagnosing, preventing and treating inflammatory disorders or
CC   disorders associated with inappropriate apoptosis, such as: inflammatory
CC   bowel disease, rheumatoid arthritis, diabetes, multiple sclerosis,
CC   Grave's disease, contact dermatitis, psoriasis, graft rejection, asthma,
CC   allergy, chronic obstructive pulmonary disease, glomerulonephritis,
CC   infections, Alzheimer's disease, Parkinson's disease, anaemia and
CC   ischaemia. The DNA and protein sequences of the invention may also be
CC   used in screening assays, chromosomal mapping, tissue typing, forensic
CC   biology, pharmacogenomics, predictive medicine, and in monitoring of
CC   clinical trials. The present DNA sequence encodes a PYRIN protein of the
CC   invention.
XX
SQ   Sequence 4035 BP; 935 A; 1022 C; 1175 G; 903 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 4035;  DB 10;  Length 4035;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300

Qy        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360

Qy        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420

Qy        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480

Qy        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540

Qy        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

Qy        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140
Qy       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200
Db       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200
Qy       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260
Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260
Qy       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320
Db       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320
Qy       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380
Db       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380
Qy       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440
Db       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440
Qy       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500
Db       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500
Qy       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560
Db       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560
Qy       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
Db       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
Qy       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680
Db       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680
Qy       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740
Db       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740
Qy       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800
Db       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800
Qy       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860
Db       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860
Qy       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
Db       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
Qy       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
Db       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
Qy       1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
Db       1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
Qy       2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Db       2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Qy       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Db       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Qy       2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
Db       2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
Qy       2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
Db       2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
Qy       2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
Db       2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
Qy       2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
Db       2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
Qy       2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
Db       2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
Qy       2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520
Db       2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520
Qy       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
Db       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
Qy       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Db       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Qy       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Db       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Qy       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Db       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Qy       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
Db       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
Qy       2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880
Db       2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880
Qy       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
Db       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
Qy       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
Db       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
Qy       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Db       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Qy       3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
Db       3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
Qy       3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
Db       3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
Qy       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
Db       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
Qy       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
Db       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
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Qy       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360

Qy       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420

Qy       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480

Qy       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540

Qy       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600

Qy       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660

Qy       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720

Qy       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780

Qy       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840

Qy       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900

Qy       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960

Qy       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020

Qy       4021 GGGCTGGTGTCTTAA 4035
             ||||||||||||||||
Db       4021 GGGCTGGTGTCTTAA 4035
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RESULT 3
ABK48628
ID   ABK48628 standard; cDNA; 3900 BP.
XX
AC   ABK48628;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Human MATER cDNA.
XX
KW   Human; gene; ss; contraceptive; antiinfertility; MATER;
KW   maternal antigen that embryos require; MATER null phenotype; oocyte;
KW   early embryonic survival; premature ovarian failure; POF;
KW   autoimmune infertility; chromosome 19; gene therapy; fertility.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3603
FT                   /*tag=  a
FT                   /product= "Human MATER"
XX
PN   WO200232955-A1.
XX
PD   25-APR-2002.
XX
PF   04-APR-2001; 2001WO-US010981.
XX
PR   18-OCT-2000; 2000US-0241510P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nelson LM,  Tong Z;
XX
DR   WPI; 2002-454595/48.
DR   P-PSDB; AAU79526.
XX
PT   New isolated human Maternal Antigen That Embryos Require protein and
PT   polynucleotide, useful in diagnosing or treating fertility or reduced
PT   fertility, or as a contraceptive.
XX
PS   Claim 11; Page 80-85; 93pp; English.
XX
CC   The invention discloses an isolated human MATER (Maternal Antigen That
CC   Embryos Require) protein, which can complement a MATER null phenotype in
CC   which zygotes arising from the oocyte do not progress beyond the two-cell
CC   stage. MATER is required for early embryonic survival and abnormal levels
CC   of the protein can lead to premature ovarian failure (POF) and can be
CC   caused by under or over expression of MATER or an autoimmune response to
CC   MATER. MATER is a single-copy maternal effect gene found on chromosome
CC   19. The MATER protein and polynucleotide, by gene therapy, are useful in
CC   diagnosing or treating fertility and reduced fertility. In particular,
CC   the MATER protein is useful as a contraceptive agent, or for influencing
CC   (either inhibiting or enhancing) fertility and can be used to detect a
CC   predisposition to infertility or reduced fertility, or for presymptomatic
CC   screening of an individual for infertility/reduced fertility. The protein
CC   and polynucleotide are also useful for detecting an excess or deficiency,
CC   or genetic mutation, of the MATER protein in a mammalian subject (e.g. a
CC   human or a mouse) or for screening for a compound useful in influencing
CC   MATER-mediated fertility. The sequence presented is the human MATER cDNA.
CC   Note: Nucleotides 1-75 were deduced, by the inventors, by comparison to
CC   published human genomic DNA sequences, while the remainder of the
CC   sequence was determined by direct cloning of human ovarian cDNAs
XX
SQ   Sequence 3900 BP; 981 A; 987 C; 1044 G; 888 T; 0 U; 0 Other;
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  Query Match             78.5%;  Score 3166.2;  DB 6;  Length 3900;
  Best Local Similarity   96.2%;  Pred. No. 0;
  Matches 3304;  Conservative    0;  Mismatches    8;  Indels  123;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 213

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 273

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 393

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453

Qy        290 ---------------------------------------------------------- 289

Db        454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513
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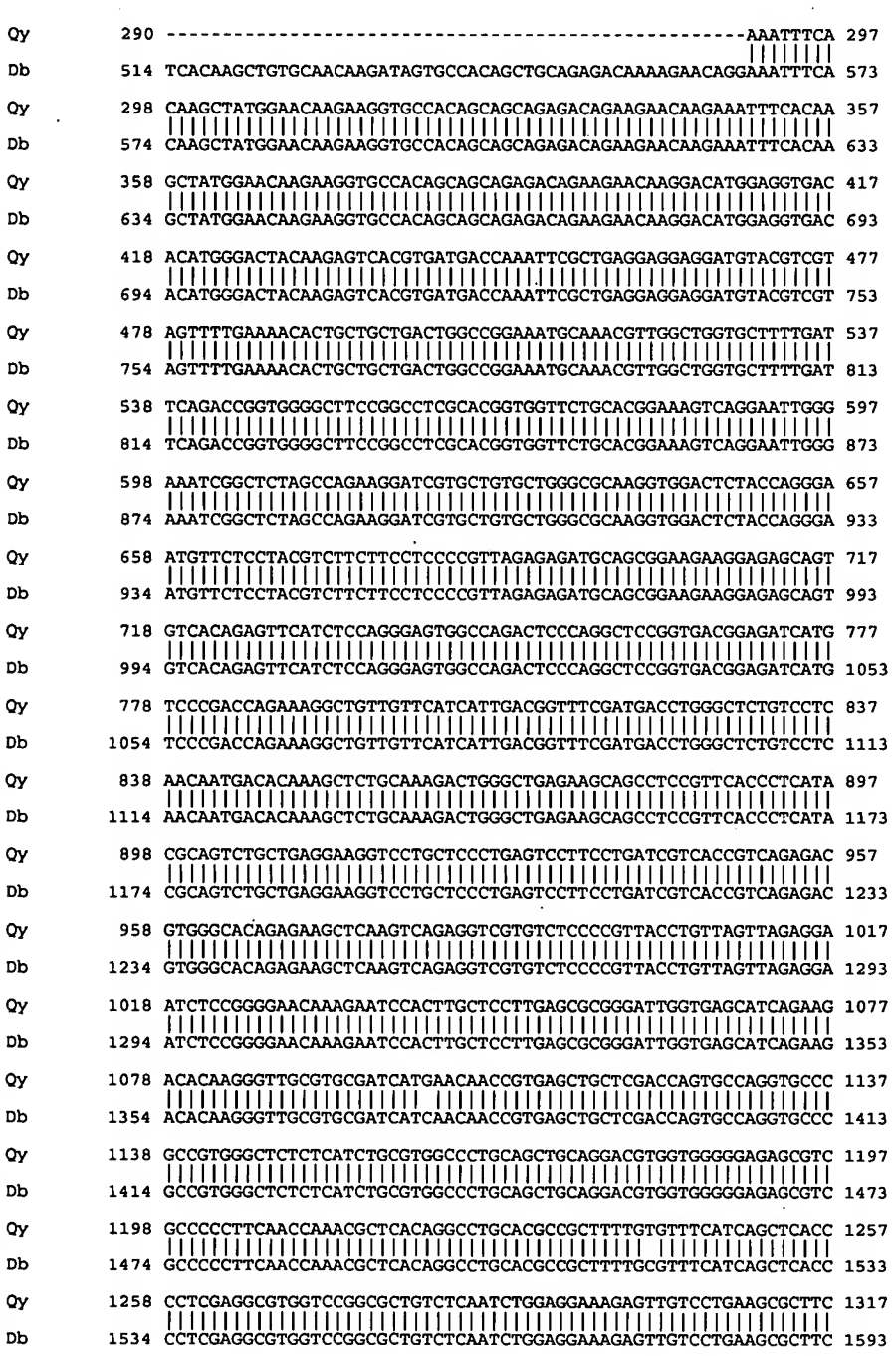
Qy 290 ----------AAATTTCA 297
Db 514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573
Qy 298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
Db 574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633
Qy 358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
Db 634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693
Qy 418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
Db 694 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 753
Qy 478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
Db 754 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 813
Qy 538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
Db 814 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 873
Qy 598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
Db 874 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 933
Qy 658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
Db 934 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 993
Qy 718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
Db 994 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 1053
Qy 778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
Db 1054 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 1113
Qy 838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
Db 1114 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 1173
Qy 898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
Db 1174 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 1233
Qy 958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
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Qy 1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
Db 1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353
Qy 1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
Db 1354 ACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1413
Qy 1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
Db 1414 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1473
Qy 1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
Db 1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533
Qy 1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
Db 1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593
Qy 1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
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Qy 1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
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Qy 1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
Db 1714 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1773
Qy 1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
Db 1774 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1833
Qy 1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
Db 1834 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1893
Qy 1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
Db 1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953
Qy 1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
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Qy 1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
Db 2014 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 2073
Qy 1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
Db 2074 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 2133
Qy 1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
Db 2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193
Qy 1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
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Qy 1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
Db 2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313
Qy 2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
Db 2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373
Qy 2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
Db 2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433
Qy 2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
Db 2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493
Qy 2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
Db 2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553
Qy 2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
Db 2554 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2613
Qy 2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
Db 2614 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2673
Qy 2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457

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Db       2674 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2733

Qy       2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517
              | |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       2734 ACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2793

Qy       2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2913

Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2973

Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       2974 CTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 3033

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 3213

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3334 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3393

Qy       3118 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3453

Qy       3178 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3513

Qy       3238 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3573

Qy       3298 GAAGATGACCGACAC 3312
              |||||||||| ||
Db       3574 GAAGATGACCGGTAC 3588


RESULT 4
AAD49018
ID   AAD49018 standard; cDNA; 3900 BP.
XX
AC   AAD49018;
XX
DT   07-MAR-2003  (first entry)
XX
DE   Human MATER cDNA.
XX
KW   Human; MATER protein; infertility; fertility; contraceptive agent;
KW   gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3603
FT                   /*tag=  a
FT                   /product= "Human MATER protein"
XX
PN   WO200281492-A1.
XX
PD   17-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-US009776.
XX
PR   04-APR-2001; 2001WO-US010981.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nelson LM,  Tong Z;
XX
DR   WPI; 2003-058494/05.
DR   P-PSDB; AAE31749.
XX
PT   New isolated variant MATER proteins and nucleic acids, useful for
PT   diagnosing, prognosing and treating infertility and reduced fertility,
PT   and as contraceptive agents.
XX
PS   Example 2; Page 93-98; 110pp; English.
XX
CC   The present invention relates to novel MATER proteins and polynucleotides
CC   encoding such proteins. The MATER proteins are essential to fertility.
CC   Sequences of the invention are useful for diagnosing, prognosing and
CC   treating infertility, reduced fertility and as contraceptive agents. They
CC   are also useful in gene therapy. The method is useful for detecting a
CC   predisposition to or pre-symptomatic screening of an individual for
CC   infertility or reduced fertility. The present sequence is human MATER
CC   cDNA
XX
SQ   Sequence 3900 BP; 981 A; 987 C; 1044 G; 888 T; 0 U; 0 Other;

  Query Match             78.5%;  Score 3166.2;  DB 8;  Length 3900;
  Best Local Similarity   96.2%;  Pred. No. 0;
  Matches 3304;  Conservative    0;  Mismatches    8;  Indels  123;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 213

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 273

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 393

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453

Qy        290 --------------------------------------------------------- 289

Db        454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513

Qy        290 ----------------------------------------------------AAATTTCA 297
                                                                 ||||||||
```

```
Db        514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573
Qy        298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633
Qy        358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693
Qy        418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 753
Qy        478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 813
Qy        538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 873
Qy        598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 933
Qy        658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 993
Qy        718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 1053
Qy        778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 1113
Qy        838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 1173
Qy        898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 1233
Qy        958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1234 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1293
Qy       1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353
Qy       1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1354 ACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1413
Qy       1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1414 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1473
Qy       1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533
Qy       1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593
Qy       1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1594 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1653

Qy       1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1654 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1713
Qy       1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1714 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1773
Qy       1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1774 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1833
Qy       1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1834 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1893
Qy       1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953
Qy       1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1954 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 2013
Qy       1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2014 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 2073
Qy       1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2074 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 2133
Qy       1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193
Qy       1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2194 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 2253
Qy       1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313
Qy       2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373
Qy       2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433
Qy       2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493
Qy       2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553
Qy       2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2554 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2613
Qy       2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2614 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2673
Qy       2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2674 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2733
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Qy       2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517
             | ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       2734 ACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2793

Qy       2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2913

Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2973

Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       2974 CTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 3033

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 3213

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3334 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3393

Qy       3118 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3453

Qy       3178 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3237
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3513

Qy       3238 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3514 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3573

Qy       3298 GAAGATGACCGACAC 3312
             ||||||||||| ||
Db       3574 GAAGATGACCGGTAC 3588
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RESULT 5
ADA45220
ID   ADA45220 standard; DNA; 3830 BP.
XX
AC   ADA45220;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MATER splice variant DNA SEQ ID 3.
XX
KW   human; MATER; maternal antigen that embryos require; NTP-ase;
KW   nucleoside triphosphate-ase; apoptosis; antiinfertility; contraceptive;
KW   antiinflammatory; immunosuppressive; gynaecological; endometriosis;
KW   ovarian dysfunction; autoimmune premature ovarian failure;
KW   autoimmune disease; contraceptive; autoantibody; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3432
FT                   /*tag= a
FT                   /product= "splice variant of MATER"
XX
PN   EP1285964-A2.
XX
PD   26-FEB-2003.
XX
PF   12-JUL-2002; 2002EP-00090246.
XX
PR   10-AUG-2001; 2001DE-01039874.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Weiss B,  Lessl M,  Peters-Kottig M,  Beckmann G;
XX
DR   WPI; 2003-302814/30.
DR   P-PSDB; ADA45221.
XX
PT   New nucleic acid for human maternal antigen that embryos require protein,
PT   useful e.g. in diagnosis and treatment of female infertility.
XX
PS   Claim 1; Page 17-18; 31pp; German.
XX
CC   This invention describes a novel human MATER (maternal antigen that
CC   embryos require) protein. MATER is an NTP(nucleoside triphosphate)-ase
CC   associated with apoptosis, a defect in MATER activity causes growth
CC   arrest at the 2-cell stage of fertilized eggs. mRNA transcribed from the
CC   MATER gene is found predominantly in ovary, testis and placenta. The
CC   products of the invention have antiinfertility, contraceptive,
CC   antiinflammatory, immunosuppressive and gynaecological activity.
CC   Effectors of the MATER polypeptide are used to treat infertility
CC   associated with endometriosis and also ovarian dysfunction, autoimmune
CC   premature ovarian failure, inflammation, autoimmune diseases and female
CC   infertility, and as contraceptives. Measurements of autoantibodies
CC   against MATER in body samples or MATER protein or mRNA in eggs is useful
CC   for diagnosis of female infertility, particularly by detecting mutations
CC   in the MATER gene with a DNA chip. This sequence represents a splice
CC   variant of human MATER in which exon 4 of the usual form is absent.
XX
SQ   Sequence 3830 BP; 943 A; 946 C; 1041 G; 900 T; 0 U; 0 Other;

  Query Match            77.8%;  Score 3139;  DB 8;  Length 3830;
  Best Local Similarity  96.0%;  Pred. No. 0;
  Matches 3282;  Conservative    0;  Mismatches   30;  Indels  105;  Gaps    2;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||     || ||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300
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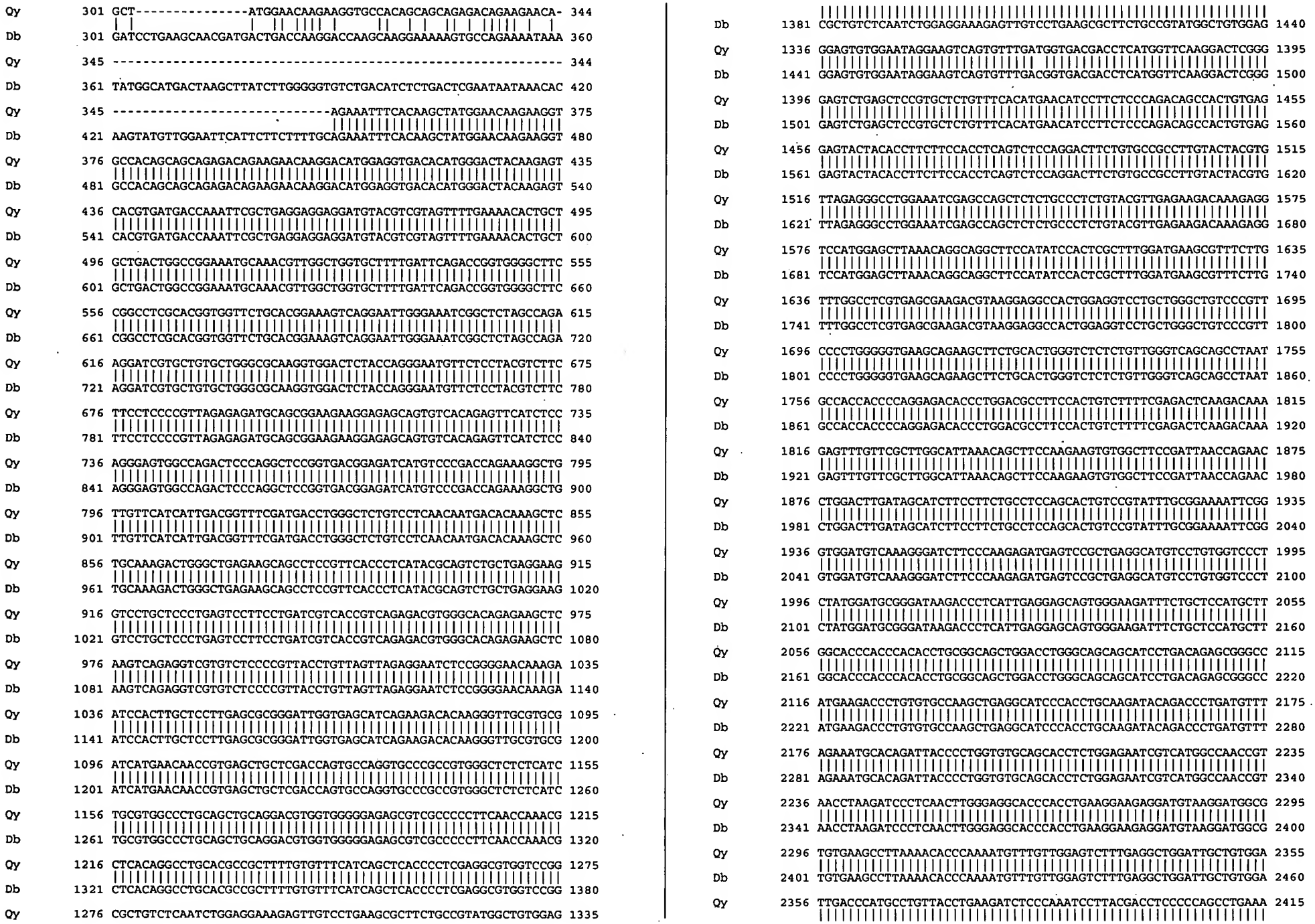

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Db       2461 TTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAA 2520

Qy       2416 TCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCC 2475
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 TCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCC 2580

Qy       2476 TTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCC 2535
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCC 2640

Qy       2536 ACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGC 2595
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 ACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGC 2700

Qy       2596 CTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTT 2655
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 CTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTT 2760

Qy       2656 CCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGT 2715
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGT 2820

Qy       2716 GGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATG 2775
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 GGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATG 2880

Qy       2776 AACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGT 2835
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 AACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGT 2940

Qy       2836 CATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTG 2895
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTG 3000

Qy       2896 TCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTG 2955
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Db       3001 TCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTG 3060

Qy       2956 GGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACG 3015
             |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       3061 GGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACG 3120

Qy       3016 AGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCC 3075
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 AGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCC 3180

Qy       3076 CTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAA 3135
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAA 3240

Qy       3136 GGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGG 3195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGG 3300

Qy       3196 CTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTC 3255
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 CTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTC 3360

Qy       3256 AAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db       3361 AAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 3417


RESULT 6
AAD41224
ID   AAD41224 standard; cDNA; 3489 BP.
XX
AC   AAD41224;
XX
DT   30-OCT-2002  (first entry)
XX
DE   Human EMBRY-1 cDNA.
XX
KW   Human; embryogenesis associated protein; AIDS; reproductive disorder;
KW   infertility; endometriosis; endometrial tumour; inflammatory disorder;
KW   autoimmune disorder; acquired immune deficiency syndrome; transgenic;
KW   ovarian tumour; contact dermatitis; placenta disorder; preeclampsia;
KW   EMBRY-1; allergy; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3489
FT                   /*tag=  a
FT                   /product= "EMBRY-1 protein"
XX
PN   WO200248362-A2.
XX
PD   20-JUN-2002.
XX
PF   14-NOV-2001; 2001WO-US043956.
XX
PR   15-NOV-2000; 2000US-0249407P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Ramkumar J,  Arvizu C;
XX
DR   WPI; 2002-537629/57.
DR   P-PSDB; AAE25053.
XX
PT   New polypeptides of human embryogenesis associated proteins for screening
PT   modulators useful for treating or preventing disorders e.g.
PT   endometriosis, infertility, allergy, preeclampsia.
XX
PS   Claim 58; Page 95-96; 97pp; English.
XX
CC   The invention relates to human embryogenesis associated proteins (EMBRY)
CC   and nucleic acid molecules encoding such proteins. EMBRY sequences are
CC   useful for screening modulators useful for treating or preventing
CC   disorders associated with abnormal expression of EMBRY. The disorders
CC   treated include reproductive disorders such as infertility,
CC   endometriosis, endometrial or ovarian tumour; autoimmune/inflammatory
CC   disorder such as acquired immune deficiency syndrome (AIDS), allergies,
CC   contact dermatitis; disorders of the placenta such as preeclampsia,
CC   abruptio placentae etc. Sequences of the invention are also useful for
CC   analysing a proteome of a tissue or a cell type. EMBRY proteins are
CC   useful as immunogens for preparing antibodies. Polynucleotides of the
CC   invention are useful for creating knockin humanised animals or transgenic
CC   animals to model human diseases. They are also used in gene therapy. The
CC   present sequence is human EMBRY-1 cDNA
XX
SQ   Sequence 3489 BP; 854 A; 881 C; 961 G; 793 T; 0 U; 0 Other;

  Query Match          77.7%;  Score 3133.6;  DB 6;  Length 3489;
  Best Local Similarity   95.2%;  Pred. No. 0;
  Matches 3308;  Conservative    0;  Mismatches    4;  Indels  162;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300
Qy       290 ------------------------------------------------------------ 289
Db       301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360
Qy       290 ------------------------------------------------------------ 289
Db       361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420
Qy       290 ------------------------------AAATTTCACAAGCTATGGAACAAGAAGGT 318
                                            ||||||||||||||||||||||||||||||
Db       421 AAGTATGTTGGAATTCATTCTTCTTTTGCAGAAATTTCACAAGCTATGGAACAAGAAGGT 480
Qy       319 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 540
Qy       379 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 438
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 600
Qy       439 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 498
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 660
Qy       499 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 558
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 720
Qy       559 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 618
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 780
Qy       619 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 678
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 840
Qy       679 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 738
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 900
Qy       739 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 798
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 960
Qy       799 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 858
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 1020
Qy       859 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 918
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 1080
Qy       919 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 978
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 1140
Qy       979 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATC 1038
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATC 1200
Qy      1039 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1098
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1260
Qy      1099 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1158
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1320
Qy      1159 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1218
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1380

Qy      1219 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1278
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1440
Qy      1279 TGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGA 1338
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 TGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGA 1500
Qy      1339 GTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1398
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 GTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1560
Qy      1399 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1458
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1620
Qy      1459 TACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTA 1518
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 TACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTA 1680
Qy      1519 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1578
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1740
Qy      1579 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1638
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1800
Qy      1639 GGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCC 1698
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 GGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCC 1860
Qy      1699 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1920
Qy      1759 ACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAG 1818
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 ACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAG 1980
Qy      1819 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 1878
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 2040
Qy      1879 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 1938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 2100
Qy      1939 GATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTA 1998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 GATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTA 2160
Qy      1999 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2220
Qy      2059 ACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATG 2118
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 ACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATG 2280
Qy      2119 AAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGA 2178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 AAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGA 2340
Qy      2179 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2400
Qy      2239 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2460
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Qy       2299 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2520

Qy       2359 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2580

Qy       2419 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2478
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2640

Qy       2479 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2700

Qy       2539 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2598
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2760

Qy       2599 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2820

Qy       2659 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2880

Qy       2719 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2940

Qy       2779 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 2838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 3000

Qy       2839 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 2898
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Db       3001 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 3060

Qy       2899 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 2958
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Db       3061 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 3120

Qy       2959 GACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3018
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3180

Qy       3019 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3240

Qy       3079 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3300

Qy       3139 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3198
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Db       3301 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3360

Qy       3199 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3258
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Db       3361 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3420

Qy       3259 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
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Db       3421 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 3474
```

```
RESULT 7
ADA45218
ID   ADA45218 standard; DNA; 3926 BP.
XX
AC   ADA45218;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MATER DNA.
XX
KW   human ; MATER; maternal antigen that embryos require; NTP-ase;
KW   nucleoside triphosphate-ase; apoptosis; antiinfertility; contraceptive;
KW   antiinflammatory; immunosuppressive; gynaecological; endometriosis;
KW   ovarian dysfunction; autoimmune premature ovarian failure;
KW   autoimmune disease; contraceptive; autoantibody; ds; gene.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .3489
FT                   /*tag=  a
FT                   /product= "MATER"
XX
PN   EP1285964-A2.
XX
PD   26-FEB-2003.
XX
PF   12-JUL-2002; 2002EP-00090246.
XX
PR   10-AUG-2001; 2001DE-01039874.
XX
PA   (SCHD ) SCHERING AG.
XX
PI   Weiss B,  Lessl M,  Peters-Kottig M,  Beckmann G;
XX
DR   WPI; 2003-302814/30.
DR   P-PSDB; ADA45219.
XX
PT   New nucleic acid for human maternal antigen that embryos require protein,
PT   useful e.g. in diagnosis and treatment of female infertility.
XX
PS   Claim 1; Page 9-11; 31pp; German.
XX
CC   This invention describes a novel human MATER (maternal antigen that
CC   embryos require) protein. MATER is an NTP(nucleoside triphosphate)-ase
CC   associated with apoptosis, a defect in MATER activity causes growth
CC   arrest at the 2-cell stage of fertilized eggs. mRNA transcribed from the
CC   MATER gene is found predominantly in ovary, testis and placenta. The
CC   products of the invention have antiinfertility, contraceptive,
CC   antiinflammatory, immunosuppressive and gynaecological activity.
CC   Effectors of the MATER polypeptide are used to treat infertility
CC   associated with endometriosis and also ovarian dysfunction, autoimmune
CC   premature ovarian failure, inflammation, autoimmune diseases and female
CC   infertility, and as contraceptives. Measurements of autoantibodies
CC   against MATER in body samples or MATER protein or mRNA in eggs is useful
CC   for diagnosis of female infertility, particularly by detecting mutations
CC   in the MATER gene with a DNA chip. This sequence encodes the human MATER
CC   polypeptide described in the invention.
XX
SQ   Sequence 3926 BP; 969 A; 958 C; 1061 G; 938 T; 0 U; 0 Other;

  Query Match             77.7%;  Score 3133.6;  DB 8;  Length 3926;
  Best Local Similarity   95.2%;  Pred. No. 0;
  Matches 3308;  Conservative    0;  Mismatches    4;  Indels  162;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
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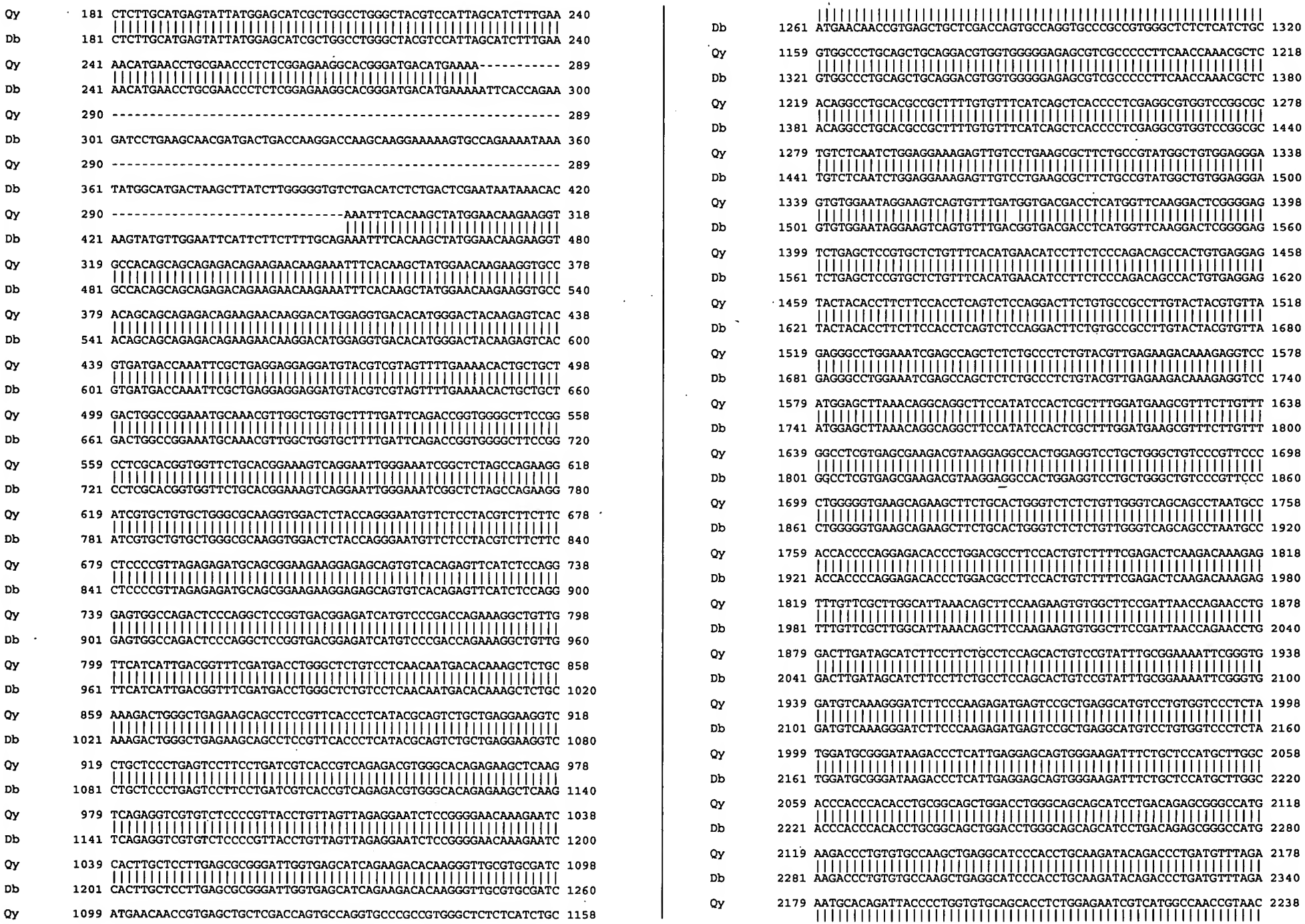

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Db       2341 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2400

Qy       2239 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2460

Qy       2299 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2520

Qy       2359 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2580

Qy       2419 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2478
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Db       2581 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2640

Qy       2479 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2700

Qy       2539 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2598
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2760

Qy       2599 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2820

Qy       2659 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2880

Qy       2719 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2940

Qy       2779 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 2838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 3000

Qy       2839 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 2898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 3060

Qy       2899 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 2958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 3120

Qy       2959 GACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3018
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3180

Qy       3019 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3240

Qy       3079 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3300

Qy       3139 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3360

Qy       3199 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3420

Qy       3259 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
             ||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db       3421 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 3474
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RESULT 8
AAL47135
ID   AAL47135 standard; DNA; 5859 BP.
XX
AC   AAL47135;
XX
DT   20-AUG-2002  (first entry)
XX
DE   Pyrin domain containing protein NALP8/Py12 coding sequence.
XX
KW   Pyrin domain; PYD domain; antiinflammatory; antiparkinsonian;
KW   antiarteriosclerotic; antipsoriatic; antibacterial; virucide;
KW   neuroprotective; antiarthritic; antirheumatic; antiasthmatic;
KW   nephrotropic; osteopathic; nootropic; intracellular signal transduction;
KW   inflammation; Alzheimer's disease; infection; psoriasis; asthma;
KW   arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis;
KW   osteoarthritis; glomerulonephritis; gene; ds.
XX
OS   Unidentified.
XX
PN   WO200240668-A2.
XX
PD   23-MAY-2002.
XX
PF   30-OCT-2001; 2001WO-EP012545.
XX
PR   15-NOV-2000; 2000DE-01056687.
PR   30-NOV-2000; 2000DE-01059595.
XX
PA   (APOT-) APOTECH RES & DEV LTD.
XX
PI   Tschopp J,  Martinon F;
XX
DR   WPI; 2002-427093/45.
DR   P-PSDB; AAO17863.
XX
PT   New DNA encoding protein with pyrin domain, useful for treating diseases
PT   involving impaired signal transduction, particularly inflammation, also
PT   proteins and antibodies.
XX
PS   Claim 5; Fig 1; 116pp; German.
XX
CC   The present invention relates the DNA and their encoded proteins, where
CC   the proteins contain at least one PYD (pyrin) domain. These can be used
CC   to treat diseases associated with impaired intracellular signal
CC   transduction, particularly inflammation such as psoriasis,
CC   arteriosclerosis, bacterial or viral infections (particularly meningitis
CC   and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma,
CC   sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's
CC   and Parkinson's diseases. The present sequence is a coding sequence of
CC   the invention
XX
SQ   Sequence 5859 BP; 1512 A; 1443 C; 1530 G; 1374 T; 0 U; 0 Other;

  Query Match           75.8%;  Score 3057.8;  DB 6;  Length 5859;
  Best Local Similarity   96.2%;  Pred. No. 0;
  Matches 3192;  Conservative    0;  Mismatches    2;  Indels  123;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
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Db       1975 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 2034

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2035 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 2094

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2095 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 2154

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
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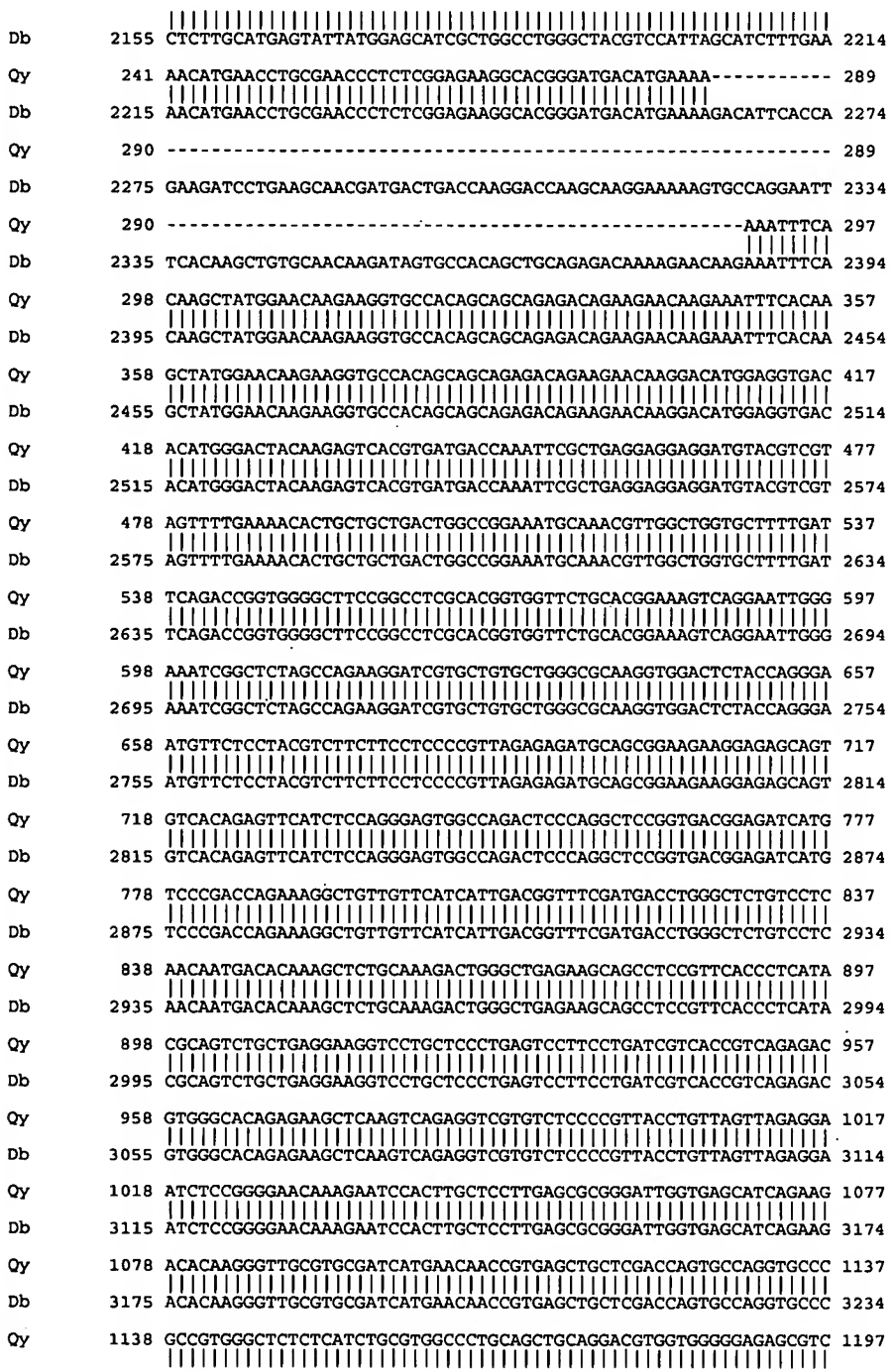
Db 2155 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 2214
Qy 241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
Db 2215 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 2274
Qy 290 ---------- 289
Db 2275 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 2334
Qy 290 ----------AAATTTCA 297
Db 2335 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAAGAAATTTCA 2394
Qy 298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
Db 2395 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 2454
Qy 358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
Db 2455 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 2514
Qy 418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
Db 2515 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 2574
Qy 478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
Db 2575 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 2634
Qy 538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
Db 2635 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 2694
Qy 598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
Db 2695 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 2754
Qy 658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
Db 2755 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 2814
Qy 718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
Db 2815 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 2874
Qy 778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
Db 2875 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 2934
Qy 838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
Db 2935 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 2994
Qy 898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
Db 2995 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 3054
Qy 958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
Db 3055 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 3114
Qy 1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
Db 3115 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 3174
Qy 1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
Db 3175 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 3234
Qy 1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
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Qy 1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
Db 3295 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 3354
Qy 1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
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Qy 1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
Db 3415 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTC 3474
Qy 1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
Db 3475 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 3534
Qy 1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
Db 3535 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 3594
Qy 1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
Db 3595 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 3654
Qy 1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
Db 3655 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 3714
Qy 1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
Db 3715 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 3774
Qy 1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
Db 3775 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 3834
Qy 1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
Db 3835 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 3894
Qy 1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
Db 3895 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 3954
Qy 1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
Db 3955 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 4014
Qy 1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
Db 4015 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 4074
Qy 1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
Db 4075 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 4134
Qy 2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
Db 4135 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 4194
Qy 2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
Db 4195 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 4254
Qy 2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
Db 4255 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 4314
Qy 2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
Db 4315 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 4374

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Qy       2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4375 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 4434

Qy       2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4435 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 4494

Qy       2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4495 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 4554

Qy       2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4555 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 4614

Qy       2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4615 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 4674

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4675 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 4734

Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4735 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 4794

Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4795 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 4854

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4855 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 4914

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4915 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 4974

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4975 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 5034

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       5035 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAA 5094

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5095 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 5154

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5155 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 5214

Qy       3118 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5215 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 5274

Qy       3178 AACTTACAGATAATTGG 3194
             |||||||||||||||||
Db       5275 AACTTACAGATAATTGG 5291
```

RESULT 9
AAL47131
ID AAL47131 standard; DNA; 6939 BP.
XX
AC AAL47131;
XX
DT 20-AUG-2002 (first entry)
XX
DE Pyrin domain containing protein NALP5/Py8-hs coding sequence.
XX
KW Pyrin domain; PYD domain; antiinflammatory; antiparkinsonian;
KW antiarteriosclerotic; antipsoriatic; antibacterial; virucide;
KW neuroprotective; antiarthritic; antirheumatic; antiasthmatic;
KW nephrotropic; osteopathic; nootropic; intracellular signal transduction;
KW inflammation; Alzheimer's disease; infection; psoriasis; asthma;
KW arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis;
KW osteoarthritis; glomerulonephritis; gene; ds.
XX
OS Unidentified.
XX
PN WO200240668-A2.
XX
PD 23-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-EP012545.
XX
PR 15-NOV-2000; 2000DE-01056687.
PR 30-NOV-2000; 2000DE-01059595.
XX
PA (APOT-) APOTECH RES & DEV LTD.
XX
PI Tschopp J, Martinon F;
XX
DR WPI; 2002-427093/45.
DR P-PSDB; AAO17859.
XX
PT New DNA encoding protein with pyrin domain, useful for treating diseases
PT involving impaired signal transduction, particularly inflammation, also
PT proteins and antibodies.
XX
PS Claim 5; Fig 1; 116pp; German.
XX
CC The present invention relates the DNA and their encoded proteins, where
CC the proteins contain at least one PYD (pyrin) domain. These can be used
CC to treat diseases associated with impaired intracellular signal
CC transduction, particularly inflammation such as psoriasis,
CC arteriosclerosis, bacterial or viral infections (particularly meningitis
CC and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma,
CC sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's
CC and Parkinson's diseases. The present sequence is a coding sequence of
CC the invention
XX
SQ Sequence 6939 BP; 1791 A; 1719 C; 1801 G; 1628 T; 0 U; 0 Other;

```
  Query Match          75.8%;  Score 3057.8;  DB 6;  Length 6939;
  Best Local Similarity  96.2%;  Pred. No. 0;
  Matches 3192;  Conservative    0;  Mismatches    2;  Indels  123;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3055 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 3114

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3115 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 3174

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3175 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 3234

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3235 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 3294

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3295 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 3354

Qy        290 ---------------------------------------------------------- 289
```

```
Db       3355 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 3414
Qy        290 ----------------------------------------------------AAATTTCA 297
                                                                   ||||||||
Db       3415 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAAGAAATTTCA 3474
Qy        298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3475 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 3534
Qy        358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3535 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 3594
Qy        418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3595 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 3654
Qy        478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3655 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 3714
Qy        538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3715 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 3774
Qy        598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3775 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 3834
Qy        658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3835 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 3894
Qy        718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3895 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 3954
Qy        778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3955 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 4014
Qy        838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4015 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 4074
Qy        898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4075 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 4134
Qy        958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4135 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 4194
Qy       1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4195 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 4254
Qy       1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4255 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 4314
Qy       1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4315 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 4374
Qy       1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4375 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 4434
Qy       1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4435 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 4494

Qy       1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
               |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db       4495 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTC 4554
Qy       1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4555 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 4614
Qy       1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4615 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 4674
Qy       1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4675 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 4734
Qy       1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4735 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 4794
Qy       1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4795 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 4854
Qy       1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4855 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 4914
Qy       1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4915 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 4974
Qy       1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4975 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 5034
Qy       1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5035 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 5094
Qy       1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5095 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 5154
Qy       1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5155 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 5214
Qy       2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5215 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 5274
Qy       2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5275 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 5334
Qy       2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5335 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 5394
Qy       2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5395 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 5454
Qy       2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5455 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 5514
Qy       2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5515 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 5574
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Qy       2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5575 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 5634

Qy       2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5635 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 5694

Qy       2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5695 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 5754

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5755 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 5814

Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5815 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 5874

Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5875 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 5934

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5935 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 5994

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5995 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 6054

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6055 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 6114

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       6115 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAA 6174

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6175 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 6234

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6235 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 6294

Qy       3118 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6295 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 6354

Qy       3178 AACTTACAGATAATTGG 3194
             |||||||||||||||||
Db       6355 AACTTACAGATAATTGG 6371
```

RESULT 10
AAL47140
ID AAL47140 standard; DNA; 6939 BP.
XX
AC AAL47140;
XX
DT 20-AUG-2002 (first entry)
XX
DE Pyrin domain containing protein NALP13/Py17 coding sequence.
XX
KW Pyrin domain; PYD domain; antiinflammatory; antiparkinsonian;
KW antiarteriosclerotic; antipsoriatic; antibacterial; virucide;
KW neuroprotective; antiarthritic; antirheumatic; antiasthmatic;
KW nephrotropic; osteopathic; nootropic; intracellular signal transduction;
KW inflammation; Alzheimer's disease; infection; psoriasis; asthma;
KW arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis;
KW osteoarthritis; glomerulonephritis; gene; ds.
XX
OS Unidentified.
XX
PN WO200240668-A2.
XX
PD 23-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-EP012545.
XX
PR 15-NOV-2000; 2000DE-01056687.
PR 30-NOV-2000; 2000DE-01059595.
XX
PA (APOT-) APOTECH RES & DEV LTD.
XX
PI Tschopp J, Martinon F;
XX
DR WPI; 2002-427093/45.
DR P-PSDB; AAO17868.
XX
PT New DNA encoding protein with pyrin domain, useful for treating diseases
PT involving impaired signal transduction, particularly inflammation, also
PT proteins and antibodies.
XX
PS Claim 5; Fig 1; 116pp; German.
XX
CC The present invention relates the DNA and their encoded proteins, where
CC the proteins contain at least one PYD (pyrin) domain. These can be used
CC to treat diseases associated with impaired intracellular signal
CC transduction, particularly inflammation such as psoriasis,
CC arteriosclerosis, bacterial or viral infections (particularly meningitis
CC and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma,
CC sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's
CC and Parkinson's diseases. The present sequence is a coding sequence of
CC the invention
XX
SQ Sequence 6939 BP; 1791 A; 1719 C; 1801 G; 1628 T; 0 U; 0 Other;

Query Match 75.8%; Score 3057.8; DB 6; Length 6939;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3192; Conservative 0; Mismatches 2; Indels 123; Gaps 1;

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Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3055 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 3114

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3115 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 3174

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3175 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 3234

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3235 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 3294

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3295 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 3354

Qy        290 ---------------------------------------------------------- 289

Db       3355 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 3414

Qy        290 ----------------------------------------------------AAATTTCA 297
                                                                   ||||||||
Db       3415 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAAGAAATTTCA 3474

Qy        298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3475 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 3534
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Qy       358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
Db      3535 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 3594

Qy       418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
Db      3595 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 3654

Qy       478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
Db      3655 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 3714

Qy       538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
Db      3715 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 3774

Qy       598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
Db      3775 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 3834

Qy       658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
Db      3835 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 3894

Qy       718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
Db      3895 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 3954

Qy       778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
Db      3955 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 4014

Qy       838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
Db      4015 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 4074

Qy       898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
Db      4075 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 4134

Qy       958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
Db      4135 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 4194

Qy      1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
Db      4195 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 4254

Qy      1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
Db      4255 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 4314

Qy      1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
Db      4315 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 4374

Qy      1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
Db      4375 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 4434

Qy      1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
Db      4435 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 4494

Qy      1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
Db      4495 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTC 4554

Qy      1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
Db      4555 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 4614

Qy      1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
Db      4615 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 4674

Qy      1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
Db      4675 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 4734

Qy      1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
Db      4735 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 4794

Qy      1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
Db      4795 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 4854

Qy      1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
Db      4855 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 4914

Qy      1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
Db      4915 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 4974

Qy      1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
Db      4975 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 5034

Qy      1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
Db      5035 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 5094

Qy      1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
Db      5095 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 5154

Qy      1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
Db      5155 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 5214

Qy      2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
Db      5215 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 5274

Qy      2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
Db      5275 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 5334

Qy      2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
Db      5335 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 5394

Qy      2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
Db      5395 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 5454

Qy      2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
Db      5455 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 5514

Qy      2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
Db      5515 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 5574

Qy      2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457
Db      5575 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 5634

Qy      2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517
Db      5635 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 5694

Qy      2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
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Db       5695 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 5754

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
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Db       5755 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 5814

Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
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Db       5815 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 5874

Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
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Db       5875 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 5934

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
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Db       5935 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 5994

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5995 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 6054

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
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Db       6055 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 6114

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
                ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       6115 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAA 6174

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6175 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 6234

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6235 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 6294

Qy       3118 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3177
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Db       6295 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 6354

Qy       3178 AACTTACAGATAATTGG 3194
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Db       6355 AACTTACAGATAATTGG 6371
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RESULT 11
ABX97181
ID ABX97181 standard; cDNA; 3226 BP.
XX
AC ABX97181;
XX
DT 20-MAY-2003 (first entry)
XX
DE Human NOV125b cDNA.
XX
KW NOVX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;
KW hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
KW human; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200272757-A2.
XX
PD 19-SEP-2002.
XX
PF 08-MAR-2002; 2002WO-US006908.
XX
PR 08-MAR-2001; 2001US-0274101P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0277338P.
PR 30-MAR-2001; 2001US-0279995P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281194P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332272P.
PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333272P.
PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
PI Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
PI Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
PI Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
PI Lepley DM, Rieger DK;
XX
DR WPI; 2002-723332/78.
DR P-PSDB; ABU65214.
XX

PT NOVX polypeptides and polynucleotides, useful for preventing or treating
PT a disorder associated with aberrant NOVX expression or activity e.g.,
PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
PT asthma.
XX
PS Claim 13; Page 467; 1103pp; English.
XX
CC This invention describes novel human NOVX polypeptides which have
CC cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive
CC activity. Pharmaceutical compositions comprising the NOVX proteins or
CC nucleic acid molecules or NOVX antibodies are useful for preventing or
CC treating a disorder associated with aberrant NOVX expression or activity
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC asthma. The products of the invention can be used for gene therapy or in
CC a vaccine. ABX97008-ABX97185 are cDNA fragments amplified and isolated by
CC the PCR primers and probes represented in ABX13460-ABX13462 and ABX97186-
CC ABX97593. ABX97008-ABX97185 encode the NOVX proteins described in
CC ABU65041-ABU65218
XX
SQ Sequence 3226 BP; 738 A; 856 C; 914 G; 718 T; 0 U; 0 Other;

Query Match 71.9%; Score 2900.6; DB 6; Length 3226;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2903; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy        406 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 308

Qy        466 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 368

Qy        526 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 428

Qy        586 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 488

Qy        646 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 548

Qy        706 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 765
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 608

Qy        766 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 668

Qy        826 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 728

Qy        886 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 788

Qy        946 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 848

Qy       1006 TTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 908

Qy       1066 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 1125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 968

Qy       1126 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         969 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1028

Qy       1186 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1029 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1088

Qy       1246 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1089 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1148

Qy       1306 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAT 1365
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Db        1149 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAC 1208

Qy       1366 GGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATG 1425
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Qy       1426 AACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTC 1485
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Qy       1606 ATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGG 1665
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Qy       1666 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1725
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Db        1509 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1568

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Db       2529 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2588

Qy       2746 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2805
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Qy       2926 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAG 2985
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RESULT 12
ADN62078
ID   ADN62078 standard; cDNA; 2820 BP.
XX
AC   ADN62078;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human cDNA encoding NOV125a.
XX
KW   Human; ss; gene; NOVX; diabetes; obesity; infectious disease; anorexia;
KW   cancer-associated cachexia; cancer; neurodegenerative disorder;
KW   Alzheimer's disease; Parkinson's disease; immune disorder;
KW   haematopoietic disorder; dyslipidaemia; chronic disease.
XX
OS   Homo sapiens.
XX
PN   US2004043382-A1.
XX
PD   04-MAR-2004.
XX
PF   07-MAR-2002; 2002US-00092900.
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PR   08-MAR-2001; 2001US-0274191P.
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PR   13-MAR-2001; 2001US-0275601P.
PR   14-MAR-2001; 2001US-0276000P.
PR   16-MAR-2001; 2001US-0276776P.
PR   19-MAR-2001; 2001US-0276994P.
PR   20-MAR-2001; 2001US-0277239P.
PR   20-MAR-2001; 2001US-0277321P.
PR   20-MAR-2001; 2001US-0277327P.
PR   20-MAR-2001; 2001US-0277338P.
PR   21-MAR-2001; 2001US-0277791P.
PR   22-MAR-2001; 2001US-0277833P.
PR   23-MAR-2001; 2001US-0278152P.
PR   26-MAR-2001; 2001US-0278894P.
PR   27-MAR-2001; 2001US-0278999P.
PR   27-MAR-2001; 2001US-0279036P.
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PR   31-JUL-2001; 2001US-0309198P.
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PR   10-SEP-2001; 2001US-0318462P.
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PR 27-SEP-2001; 2001US-0325430P.
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PR 18-OCT-2001; 2001US-0330380P.
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PR 14-NOV-2001; 2001US-0332172P.
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PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333272P.
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PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
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PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
PA (SHEN/) SHENOY S G.
PA (TAUP/) TAUPIER R J.
PA (PENA/) PENA C E A.
PA (LILL/) LI L.
PA (ZERH/) ZERHUSEN B D.
PA (GUSE/) GUSEV V Y.
PA (JIWW/) JI W.
PA (GORM/) GORMAN L.
PA (MILL/) MILLER C E.
PA (KEKU/) KEKUDA R.
PA (PATT/) PATTURAJAN M.
PA (GANG/) GANGOLLI E A.
PA (VERN/) VERNET C A M.
PA (GUOX/) GUO X S.
PA (TCHE/) TCHERNEV V T.
PA (FERN/) FERNANDES E R.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (GERL/) GERLACH V.
PA (LIUY/) LIU Y.
PA (ANDE/) ANDERSON D W.
PA (SPAD/) SPADERNA S K.
PA (CATT/) CATTERTON E.
PA (LEIT/) LEITE M W.
PA (ZHON/) ZHONG H.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
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PI Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
PI Zerhusen BD, Gusev VY, Ji W, Gorman L, Miller CE, Kekuda R;
PI Patturajan M, Gangolli EA, Vernet CAM, Guo XS, Tchernev VT;
PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y;
PI Anderson DW, Spaderna SK, Catterton E, Leite MW, Zhong H;
PI Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
DR WPI; 2004-225693/21.
DR P-PSDB; ADN62079.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for diagnosing,
PT preventing or treating NOVX-associated disorders, e.g. cancer, diabetes,
PT infection or obesity, and in chromosome mapping, tissue typing or
PT pharmacogenomics.
XX
PS Claim 17; SEQ ID NO 347; 786pp; English.
XX
CC The invention relates to an isolated polypeptide (designated NOVX, or
CC NOV1-NOV127) comprising a sequence selected from 178 fully defined amino
CC acid sequences (and their mature forms, variants and fragments). Also
CC included are an isolated nucleic acid molecule encoding NOVx, a vector
CC comprising the nucleic acid, a cell comprising the vector, methods for
CC determining the presence or amount of the polypeptide or the nucleic acid
CC molecule in a sample, methods for determining the presence of or
CC predisposition to a disease associated with altered levels of expression
CC of the above polypeptide or nucleic acid molecule in a first mammalian
CC subject, a method for identifying an agent that binds to the above
CC polypeptide, a method for identifying a potential therapeutic agent for
CC use in the treatment of a pathology that is related to aberrant
CC expression or physiological interactions of the polypeptide, a method of
CC screening for a modulator of activity or of latency or predisposition to
CC a pathology associated with the polypeptide and a method for modulating
CC the activity of the polypeptide cited above. The composition and methods
CC are useful for diagnosing, preventing or treating diseases such as
CC diabetes, obesity, infectious diseases, anorexia, cancer-associated
CC cachexia, cancer, neurodegenerative disorders like Alzheimer's disease or
CC Parkinson's disease, immune disorders, haematopoietic disorders,
CC dyslipidaemias, and other chronic diseases. These may also be used in
CC chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The polypeptides are also useful as vaccines. The
CC present sequence encodes a NOVX protein of the invention.
XX
SQ Sequence 2820 BP; 655 A; 879 C; 654 G; 632 T; 0 U; 0 Other;

Query Match 45.6%; Score 1840.6; DB 12; Length 2820;
Best Local Similarity 81.4%; Pred. No. 0;
Matches 2367; Conservative 0; Mismatches 134; Indels 406; Gaps 4;

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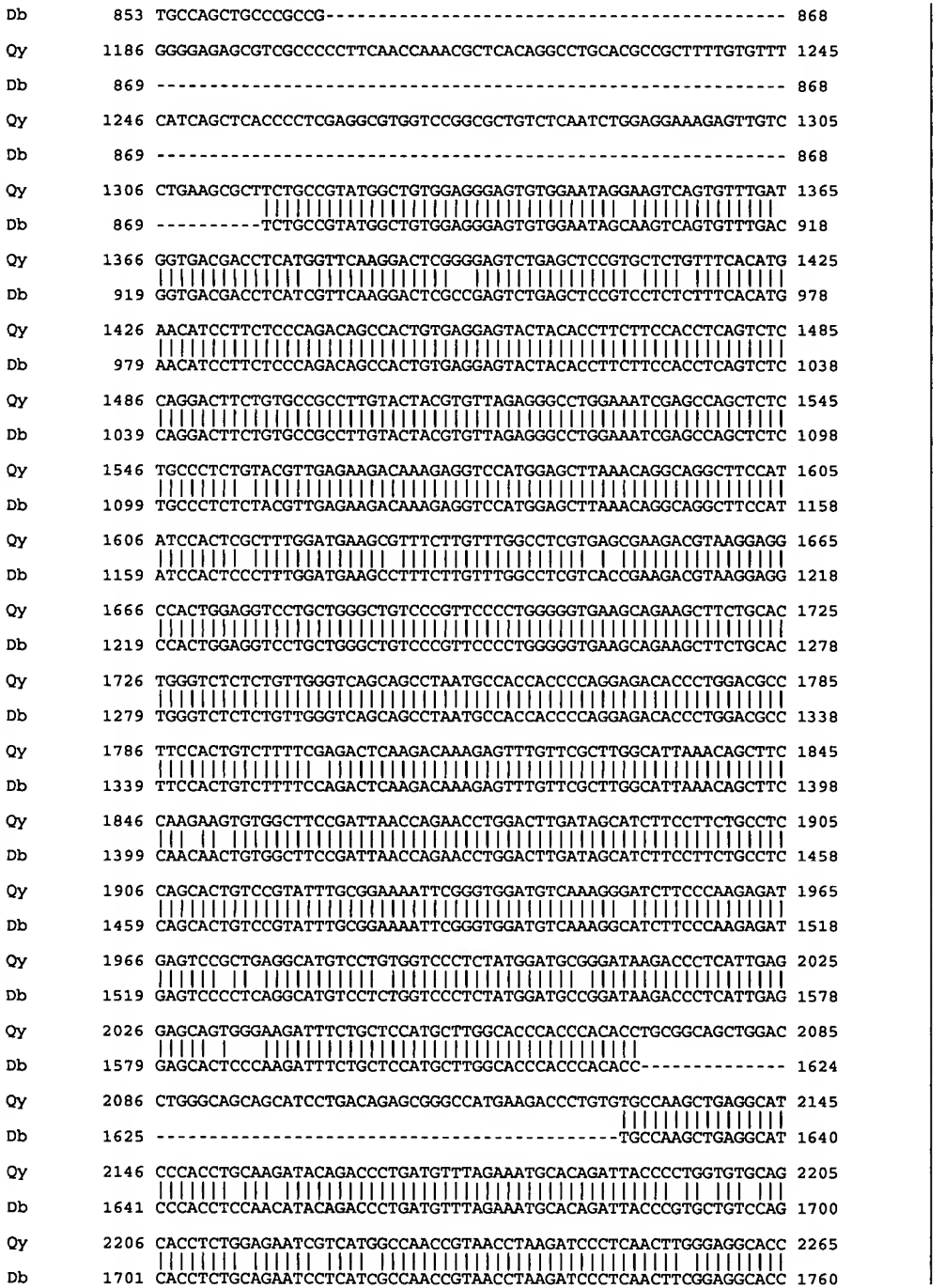
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Qy 1246 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1305
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Db 1399 CAACAACTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTC 1458
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Db 1459 CAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGCATCTTCCCAAGAGAT 1518
Qy 1966 GAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAG 2025
Db 1519 GAGTCCCCTCAGGCATGTCCTCTGGTCCCTCTATGGATGCCGGATAAGACCCTCATTGAG 1578
Qy 2026 GAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGAC 2085
Db 1579 GAGCACTCCCAAGATTTCTGCTCCATGCTTGGCACCCACCCACACC---------- 1624
Qy 2086 CTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCAT 2145
Db 1625 ----------TGCCAAGCTGAGGCAT 1640
Qy 2146 CCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAG 2205
Db 1641 CCCACCTCCAACATACAGACCCTGATGTTTAGAAATGCACAGATTACCCGTGCTGTCCAG 1700
Qy 2206 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2265
Db 1701 CACCTCTGCAGAATCCTCATCGCCAACCGTAACCTAAGATCCCTCAACTTCGGAGGCACC 1760
Qy 2266 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2325
Db 1761 CACCTCAACGAAGAGGATGTAAGGATGCCCTGTGAACCCTTAAAACACCCAAAATGTTTG 1820
Qy 2326 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2385
Db 1821 TTGGAGTCTTTGAGGCTGGATTCCTGTGGATTGACCCATGCCTGTTACCTGAACATCTCC 1880
Qy 2386 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2445
Db 1881 CAAATCCTTACGACCTCCCCCAGCCTCAAATCTCTGAGCCTGGCACGAAACAAGGTGACA 1940
Qy 2446 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAG 2505
Db 1941 CACCACGGAGTAATGCCTCTCAGTCATGCCTTGACACTCTCCCAGTGCGCCCTCCACAAG 2000
Qy 2506 CTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTC 2565
Db 2001 CTGATACTGGAGCACTCTGGCATCACACCCACGGGTTGCCAGAGTCTCGCCTCAGCCCTC 2060
Qy 2566 GTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGT 2625
Db 2061 GTCAGCAACCGGAGCTTGACACACCTGTCCCTATCCAACAACACCCTGCCGAACGAAGGT 2120
Qy 2626 GTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTG 2685
Db 2121 GTAAATCTACTCTCTCGATCCATGAGGCTTCCCCACTGTAGTCTGCACAGGCTGATGCTG 2180
Qy 2686 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2745
Db 2181 AATCAGTGCCACCTGGACACGGCTGGCTGTGCTTTTCTTGCACTTCCCCTTATGGGTAAC 2240
Qy 2746 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2805
Db 2241 TCATGCCTCACGCACCTGAGCCTTAGCATGAACCCTCTGGAAGACAATGGCCTCAACCTT 2300
Qy 2806 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2865
Db 2301 CTGTGCCAGCTCATGAGAGAACCATCTTGTCATCTCCACCACCTCCACTTGGTAAAGTCT 2360
Qy 2866 CATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTG 2925
Db 2361 CATCTCACCGCCCCGTGC---------- 2378
Qy 2926 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAG 2985
Db 2379 ----------CGGACAATGCCCTGGGTGACCCTCGCGTTCCTGCACTGTGCCAG 2422
Qy 2986 GGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACT 3045
Db 2423 CCACTGAAGCAAAACAACACTGTTCTGACCACACTCGGGTTGAAGCCATGTCCACTGACT 2482
Qy 3046 TCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTA 3105
Db 2483 TCTCATTGCTGTGAGGCACTCTCCTTCCCCCTTTCCTCCAACCGGCATCTGACCAGTCTA 2542
Qy 3106 AACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCC 3165
Db 2543 AACCTGCTGCAGAATAACTTCACTCCCAAAGGAATGATCAAGCTCTGTTCGGCCTTTCCC 2602
Qy 3166 TGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATA 3225
Db 2603 TGTCCCACGTCTAACTTACACATAATTCGCCTGTGGAAATGGCAGTACCCTGTCCAAATA 2662
Qy 3226 AGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGG 3285
Db 2663 ACCAAGCTGCTCCACCAAGTGCAGCTACTCAACCCCCGAGTCGTAATTCACGGTAGTTCG 2722
Qy 3286 CATTCTTTTGATGAAGATGACCGACAC 3312
Db 2723 CATTCTTTTCATCAACATGACCGGTAC 2749

```
RESULT 13
ABK48611
ID   ABK48611 standard; cDNA; 3447 BP.
XX
AC   ABK48611;
XX
DT   13-AUG-2002  (first entry)
XX
DE   Mouse MATER cDNA.
XX
KW   Mouse; gene; ss; contraceptive; antiinfertility; MATER;
KW   maternal antigen that embryos require; MATER null phenotype; oocyte;
KW   early embryonic survival; premature ovarian failure; POF;
KW   autoimmune infertility; gene therapy; fertility.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             9. .3344
FT                   /*tag=  a
FT                   /product= "Mouse MATER"
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PN   WO200232955-A1.
XX
PD   25-APR-2002.
XX
PF   04-APR-2001; 2001WO-US010981.
XX
PR   18-OCT-2000; 2000US-0241510P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nelson LM,  Tong Z;
XX
DR   WPI; 2002-454595/48.
DR   P-PSDB; AAU79525.
XX
PT   New isolated human Maternal Antigen That Embryos Require protein and
PT   polynucleotide, useful in diagnosing or treating fertility or reduced
PT   fertility, or as a contraceptive.
XX
PS   Example 5; Page 72-74; 93pp; English.
XX
CC   The invention discloses an isolated human MATER (Maternal Antigen That
CC   Embryos Require) protein, which can complement a MATER null phenotype in
CC   which zygotes arising from the oocyte do not progress beyond the two-cell
CC   stage. MATER is required for early embryonic survival and abnormal levels
CC   of the protein can lead to premature ovarian failure (POF) and can be
CC   caused by under or over expression of MATER or an autoimmune response to
CC   MATER. MATER is a single-copy maternal effect gene. The MATER protein and
CC   polynucleotide, by gene therapy, are useful in diagnosing or treating
CC   fertility and reduced fertility. In particular, the MATER protein is
CC   useful as a contraceptive agent, or for influencing (either inhibiting or
CC   enhancing) fertility and can be used to detect a predisposition to
CC   infertility or reduced fertility, or for presymptomatic screening of an
CC   individual for infertility/reduced fertility. The protein and
CC   polynucleotide are also useful for detecting an excess or deficiency, or
CC   genetic mutation, of the MATER protein in a mammalian subject (e.g. a
CC   human or a mouse) or for screening for a compound useful in influencing
CC   MATER-mediated fertility. The sequence presented is the mouse MATER cDNA
XX
SQ   Sequence 3447 BP; 1000 A; 783 C; 843 G; 821 T; 0 U; 0 Other;

  Query Match           31.7%;  Score 1278;  DB 6;  Length 3447;
  Best Local Similarity  67.2%;  Pred. No. 0;
  Matches 1898;  Conservative    0;  Mismatches  908;  Indels   18;  Gaps    6;

Qy        498 TGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCG 557
              |||| | || || ||| ||   ||| ||| ||||||| |  || ||| |     |||||
Db        515 TGACAGCCCAGAGATGAAATTATTGTCTGATGCTTTTAAACCATACCAGAAAACCTTCCA 574

Qy        558 GCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAG 617
              |||||| |||  |  | || || ||||  ||||| ||||||| || ||| | ||||||||
Db        575 GCCTCACACCATTATCCTACATGGAAGACCAGGAGTTGGGAAGTCAGCTTTGGCCAGAAG 634

Qy        618 GATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTT 677
              || || ||  ||||||| || |||  ||||| |||   ||||   ||||  ||| ||||
Db        635 TATTGTTCTTGGCTGGGCACAGGGTAAACTCTTCCAAAAAATG---TCCTTTGTCATCTT 691

Qy        678 CCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAG 737
              | || | |||||||| ||  || |||    || |||||||| |  || || | ||  | |
Db        692 CTTCTCTGTTAGAGAAATAAAGTGGACAGAGAAGAGCAGTTTGGCACAGCTGATTGCTAA 751

Qy        738 GGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTT 797
              |||||| |||||||||  || ||  |||||  |||||||||||| |||||||| || ||
Db        752 GGAGTGTCCAGACTCCTGGGATCTAGTGACAAAGATCATGTCCCAACCAGAAAGACTCTT 811

Qy        798 GTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC---AACAATGACACAAAGCT 854
              |||  |||| || || || |||||  ||| ||||||||||    |  |||| |  ||
Db        812 GTTTGTCATAGATGGCTTGGATGATATGGACTCTGTCCTCCAACATGATGATATGACACT 871

Qy        855 CTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAA 914
              | || |||||||   ||  | |||||   | || ||| ||   ||| || ||||||||
Db        872 ATCCAGAGACTGGAAGGATGAACAGCCCATATACATCCTGATGTACAGCCTCCTGAGGAA 931

Qy        915 GGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCT 974
              ||  ||  | ||| ||||||| || ||| | |||  |||| ||   |||  ||| || ||
Db        932 GGCTCTCTTACCTCAGTCCTTTCTCATCATTACCACCAGAAACACAGGCTTAGAAAAACT 991

Qy        975 CAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAG 1034
              |||||||  ||| |||| |||| ||  |  | |||  |||| | || |    |  ||
Db        992 CAAGTCAATGGTTGTGTCCCCCCTCTATATACTGGTTGAAGGACTGTCTGCATCAAGGAG 1051

Qy       1035 AATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGC 1094
              |   ||  || |||| ||| |        |||| | | |  | |||||  || | | |
Db       1052 ATCTCAGCTGGTCCTCGAGAACATCTCCAATGAGTCTGATAGAATACAAGTCTTCCATTC 1111

Qy       1095 GATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCAT 1154
                | ||  | || |   |||||  ||||| |||||||  ||| | ||| |||| ||  |
Db       1112 TCTGATAGAAAATCACCAGCTGTTTGACCAATGCCAGGCCCCCTCTGTGTGCTCCCTGGT 1171

Qy       1155 CTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAAC 1214
              ||| | ||| || ||||| ||| |      |||| ||||   | |||    |  ||| ||
Db       1172 CTGTGAGGCTCTACAGCTACAGAAGAAACTGGGAAAGAGATGCACCCTACCCTGCCAGAC 1231

Qy       1215 GCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCG 1274
              ||||| ||   || | ||| | || |||||||| |||||||||    | |       ||
Db       1232 TCTCACCGGTTTGTATGCCACGTTGGTGTTTCACCAGCTCACCTTGAAAAGGCCTTCCCA 1291

Qy       1275 GCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGA 1334
              | ||  |||| || ||| |||     ||   ||    | | || |||   |||| |  ||
Db       1292 GAGCGCTCTCAGTCAGGAAGAACAGATTACTCTAGTGGGTTTGTGCATGATGGCAGCTGA 1351

Qy       1335 GGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGG 1394
              ||||||||||  | || ||| |||||  ||| ||| ||||| | |    |  | ||
Db       1352 AGGAGTGTGGACCATGAGGTCGGTGTTCTATGATGATGACCTGAAGAACTATAGCCTAAA 1411

Qy       1395 GGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCC---ACTG 1451
              |||||||||| ||   || || |||||||||||||||||||||   |   |||   || |
Db       1412 GGAGTCTGAGATCTTGGCCCTCTTTCACATGAACATCCTTCTCCAGGTTGGCCACAACAG 1471

Qy       1452 TGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTA 1511
              |||| |||  ||    |||| |||||||| || ||||| |||| ||| ||||| || ||
Db       1472 TGAGCAGTGTTATGTTTTCTCCCACCTCAGCCTGCAGGATTTCTTTGCTGCCTTATATTA 1531

Qy       1512 CGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAA 1571
              || ||||| || |||||   ||    ||    |   | | |||| ||   ||
Db       1532 TGTTTTAGAAGGGCTGGA---GGAATGGAATCAGCATTTTTGCTTCATTGAAAACCAAAG 1588

Qy       1572 GAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTT 1631
              |||   |||||||  | ||    | |  |  |  |  ||  ||  ||||||||||||
Db       1589 GAGCATCATGGAGGTGAAGAGAACTGACGACACTCGCCTC---CTCGGGATGAAGCGTTT 1645

Qy       1632 CTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCC 1691
              ||| |||||||| ||| | | ||  |   || | | |||||||| ||| | |  | |||
```

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Db       1646 CTTATTTGGCCTCATGAACAAGGATATCTTGAAGACTCTGGAGGTTCTGTTTGAATATCC 1705

Qy       1692 CGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCC 1751

Db       1706 CGTGATTCCAACTGTTGAGCAGAAGCTCCAACACTGGGTCTCTCTGATAGCTCAGCAGGT 1765

Qy       1752 TAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGA 1811

Db       1766 CAATGGCACCAGCCCAATGGACACCCTGGATGCCTTCTATTGTCTATTTGAGTCTCAGGA 1825

Qy       1812 CAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCA 1871

Db       1826 TGAAGAGTTTGTTGGCGGGGCTCTCAAACGCTTCCAAGAAGTGTGGCTGCTGATTAACCA 1885

Qy       1872 GAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAAT 1931

Db       1886 GAAGATGGACTTGAAGGTCTCTTCCTACTGTCTCAAGCACTGTCAGAACTTGAAGGCAAT 1945

Qy       1932 TCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGT 1991

Db       1946 CCGGGTGGATATCAGAGACCTCCTCTCGGTAGATAATACTCTCGAGCTGTGCCCTGTTGT 2005

Qy       1992 CCCTCTATGGATGCGGGA---TAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTC 2048

Db       2006 TACTGTCCAGGAGACACAATGTAAGCCCCTCCTCATGGAGTGGTGGGGAAACTTCTGCTC 2065

Qy       2049 CATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGA 2108

Db       2066 TGTGCTTGGCAGCCTCCGGAACTTGAAGGAGCTGGACTTGGGCGACAGCATCCTGAGTCA 2125

Qy       2109 GCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCT 2168

Db       2126 ACGGGCCATGAAGATACTGTGCCTCGAGCTGCGGAATCAGTCCTGCAGAATACAGAAGCT 2185

Qy       2169 GATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGC 2228

Db       2186 GACGTTTAAGAGTGCAGAGGTAGTGTCTGGCCTGAAACATCTCTGGAAGCTCCTTTTTAG 2245

Qy       2229 CAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAG 2288

Db       2246 CAATCAAAACTTAAAGTACCTCAATCTAGGGAACACTCCCATGAAGGATGATGACATGAA 2305

Qy       2289 GATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTG 2348

Db       2306 GTTAGCCTGCGAAGCGCTGAAACATCCAAAGTGCTCCGTGGAGACTCTGAGGTTGGATTC 2365

Qy       2349 CTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAG 2408

Db       2366 CTGTGAGTTAACCATCATTGGTTATGAGATGATCTCCACGCTTCTTATTTCAACCACCAG 2425

Qy       2409 CCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAG 2468

Db       2426 GCTAAAGTGTCTCAGCCTGGCCAAAAATAGAGTGGGAGTAAAAAGCATGATATCCCTTGG 2485

Qy       2469 TGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCAT 2528

Db       2486 GAATGCCTTGAGTAGCTCAATGTGTCTACTGCAAAAGTTGATACTGGACAACTGTGGCCT 2545

Qy       2529 CACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACA 2588

Db       2546 CACACCTGCCAGCTGCCACCTTCTGGTCTCAGCCCTTTTCAGCAACCAGAACTTGACACA 2605

Qy       2589 CCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCAT 2648

Db       2606 CCTGTGCCTGTCAAACAACAGCCTGGGGACTGAAGGAGTGCAACAGCTGTGTCAGTTCCT 2665

Qy       2649 GAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGC 2708

Db       2666 GAGGAATCCAGAATGTGCTCTCCAGCGGCTGATACTGAATCACTGCAACATTGTAGATGA 2725

Qy       2709 TGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCT 2768

Db       2726 TGCTTATGGCTTCCTGGCAATGAGACTTGCAAACAACACAAAGCTGACCCACCTGAGCCT 2785

Qy       2769 TAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACC 2828

Db       2786 GACCATGAACCCCGTAGGGGATGGTGCAATGAAGCTACTGTGTGAAGCTTTAAAGGAACC 2845

Qy       2829 ATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGA 2888

Db       2846 TACTTGTTACCTTCAAGAACTGGAACTAGTGGACTGCCAACTCACACAGAACTGCTGCGA 2905

Qy       2889 GAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAA 2948

Db       2906 GGACCTGGCCTGTATGATCACAACAACCAAGCACTTAAAAAGTTTGGATCTTGGTAACAA 2965

Qy       2949 TGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGT 3008

Db       2966 CGCCCTGGGTGACAAAGGAGTCATAACCCTGTGTGAGGGACTGAAGCAAAGTAGCAGCTC 3025

Qy       3009 TCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTC 3068

Db       3026 CCTGAGGAGACTTGGGTTGGGGGCATGTAAGTTGACTTCCAATTGCTGTGAGGCATTGTC 3085

Qy       3069 CTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAG 3128

Db       3086 ATTGGCCATCTCTTGCAACCCTCACCTGAACAGCCTAAACCTGGTGAAGAATGACTTCAG 3145

Qy       3129 TCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGAT 3188

Db       3146 TACATCGGGGATGTTGAAGCTGTGCTCTGCGTTCCAATGCCCTGTCTCTAACCTGGGGAT 3205

Qy       3189 AATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCA 3248

Db       3206 AATTGGCCTGTGGAAGCAGGAGTACTATGCCCGAGTGAGAAGACAGCTGGAGGAAGTTGA 3265

Qy       3249 GCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 3308

Db       3266 GTTTGTCAAGCCCCACGTGGTGATTGATGGTGATTGGTATGCTAGTGATGAAGATGACCG 3325

Qy       3309 ACAC 3312

Db       3326 AAAC 3329
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RESULT 14
AAD49001
ID AAD49001 standard; cDNA; 3447 BP.
XX
AC AAD49001;
XX
DT 07-MAR-2003 (first entry)
XX
DE Mouse MATER cDNA.
XX
KW Mouse; MATER protein; infertility; fertility; contraceptive agent;
KW gene therapy; gene; ss.
XX
OS Mus sp.
XX

FH	Key	Location/Qualifiers
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FT		/transl_except= (pos:714. .716, aa:Thr)
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FT                   /transl_except= (pos:3330. .3332, aa:Thr)
FT                   /transl_except= (pos:3333. .3335, aa:Thr)
FT                   /note= "No start and stop codon"
FT                   /partial
XX
PN   WO200281492-A1.
XX
PD   17-OCT-2002.
XX
PF   29-MAR-2002; 2002WO-US009776.
XX
PR   04-APR-2001; 2001WO-US010981.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Nelson LM,  Tong Z;
XX
DR   WPI; 2003-058494/05.
DR   P-PSDB; AAE31748.
XX
PT   New isolated variant MATER proteins and nucleic acids, useful for
PT   diagnosing, prognosing and treating infertility and reduced fertility,
PT   and as contraceptive agents.
XX
PS   Example 22; Page 83-85; 110pp; English.
XX
CC   The present invention relates to novel MATER proteins and polynucleotides
CC   encoding such proteins. The MATER proteins are essential to fertility.
CC   Sequences of the invention are useful for diagnosing, prognosing and
CC   treating infertility, reduced fertility and as contraceptive agents. They
CC   are also useful in gene therapy. The method is useful for detecting a
CC   predisposition to or pre-symptomatic screening of an individual for
CC   infertility or reduced fertility. The present sequence is mouse MATER
CC   cDNA
XX
SQ   Sequence 3447 BP; 1000 A; 783 C; 843 G; 821 T; 0 U; 0 Other;

  Query Match             31.7%;  Score 1278;  DB 8;  Length 3447;
  Best Local Similarity   67.2%;  Pred. No. 0;
  Matches 1898;  Conservative    0;  Mismatches  908;  Indels   18;  Gaps    6;

Qy        498 TGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCG 557
              |||| | || || ||| ||   ||| ||| ||||||| |  || ||| |      |||||
Db        515 TGACAGCCCAGAGATGAAATTATTGTCTGATGCTTTTAAACCATACCAGAAAACCTTCCA 574

Qy        558 GCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAG 617
              ||||| ||| |  | || || ||||   ||||| ||||||| || ||| | ||||||||
Db        575 GCCTCACACCATTATCCTACATGGAAGACCAGGAGTTGGGAAGTCAGCTTTGGCCAGAAG 634

Qy        618 GATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTT 677
              || || ||  ||||||| || |||  ||||| |||   ||||   ||||  ||| ||||
Db        635 TATTGTTCTTGGCTGGGCACAGGGTAAACTCTTCCAAAAAATG---TCCTTTGTCATCTT 691

Qy        678 CCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAG 737
              | || | |||||||| ||  || |||   || |||||||| |  || || | ||  | |
Db        692 CTTCTCTGTTAGAGAAATAAAGTGGACAGAGAAGAGCAGTTTGGCACAGCTGATTGCTAA 751

Qy        738 GGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTT 797
              |||||| |||||||||  || ||  |||||  |||||||||||| |||||||||  || ||
Db        752 GGAGTGTCCAGACTCCTGGGATCTAGTGACAAAGATCATGTCCCAACCAGAAAGACTCTT 811

Qy        798 GTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC---AACAATGACACAAAGCT 854
              |||  |||| || || || |||||  ||| ||||||||||     |  |||| |  |  ||
Db        812 GTTTGTCATAGATGGCTTGGATGATATGGACTCTGTCCTCCAACATGATGATATGACACT 871

Qy        855 CTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAA 914
              | || |||||||   ||  | |||||     | || ||| ||   ||| || ||||||||
Db        872 ATCCAGAGACTGGAAGGATGAACAGCCCATATACATCCTGATGTACAGCCTCCTGAGGAA 931

Qy        915 GGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCT 974
              ||  ||  | ||| ||||||| || ||| | |||  |||| ||   |||  ||| || ||
Db        932 GGCTCTCTTACCTCAGTCCTTTCTCATCATTACCACCAGAAACACAGGCTTAGAAAAACT 991

Qy        975 CAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAG 1034
              |||||||  ||| ||||| ||||  ||  |  | |||  |||| | || |     |  ||
Db        992 CAAGTCAATGGTTGTGTCCCCCCTCTATATACTGGTTGAAGGACTGTCTGCATCAAGGAG 1051

Qy       1035 AATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGC 1094
              |   ||  || |||| |||  |          ||||  | | |  | |||||  || | | |
Db       1052 ATCTCAGCTGGTCCTCGAGAACATCTCCAATGAGTCTGATAGAATACAAGTCTTCCATTC 1111

Qy       1095 GATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCAT 1154
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Qy       1155 CTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAAC 1214
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Db       1172 CTGTGAGGCTCTACAGCTACAGAAGAAACTGGGAAAGAGATGCACCCTACCCTGCCAGAC 1231

Qy       1215 GCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCG 1274
              |||||  ||  || | ||| | || |||||||| |||||||||       | |       ||
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Qy       1275 GCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGA 1334
              | ||  ||||| || ||| |||      ||    ||    | | || |||   |||||  |  ||
Db       1292 GAGCGCTCTCAGTCAGGAAGAACAGATTACTCTAGTGGGTTTGTGCATGATGGCAGCTGA 1351

Qy       1335 GGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGG 1394
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Qy       1395 GGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCC---ACTG 1451
              ||||||||||  ||    || || |||||||||||||||||||||  |   |||   || |
Db       1412 GGAGTCTGAGATCTTGGCCCTCTTTCACATGAACATCCTTCTCCAGGTTGGCCACAACAG 1471

Qy       1452 TGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTA 1511
              |||| |||  ||    |||| |||||||||  || |||||  |||| |||  ||||| || ||
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Qy       1512 CGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAA 1571
              || ||||| || |||||    ||      ||        |   | | |||| ||   ||
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Qy       1572 GAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTT 1631
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Qy       1632 CTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCC 1691
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Qy       1692 CGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCC 1751
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Qy       1752 TAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGA 1811
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              |||  |||||||||  |  |||||| ||| ||| |||||||||  | |  |||  |  |||
Db       1886 GAAGATGGACTTGAAGGTCTCTTCCTACTGTCTCAAGCACTGTCAGAACTTGAAGGCAAT 1945

Qy       1932 TCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGT 1991
              |||||||||  ||| ||   ||  ||  |||| |  |    |||   ||  ||||| ||
Db       1946 CCGGGTGGATATCAGAGACCTCCTCTCGGTAGATAATACTCTCGAGCTGTGCCCTGTTGT 2005

Qy       1992 CCCTCTATGGATGCGGGA---TAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTC 2048
              ||  |   |  |  |||| ||||| |  |||| |||||  | |  ||||||||
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Qy       2049 CATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGA 2108
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Qy       2109 GCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCT 2168
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Qy       2169 GATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGC 2228
Db       2186 GACGTTTAAGAGTGCAGAGGTAGTGTCTGGCCTGAAACATCTCTGGAAGCTCCTTTTTAG 2245

Qy       2229 CAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAG 2288
Db       2246 CAATCAAAACTTAAAGTACCTCAATCTAGGGAACACTCCCATGAAGGATGATGACATGAA 2305

Qy       2289 GATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTG 2348
Db       2306 GTTAGCCTGCGAAGCGCTGAAACATCCAAAGTGCTCCGTGGAGACTCTGAGGTTGGATTC 2365

Qy       2349 CTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAG 2408
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Qy       2529 CACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACA 2588
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Qy       2709 TGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCT 2768
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Qy       2769 TAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACC 2828
Db       2786 GACCATGAACCCCGTAGGGGATGGTGCAATGAAGCTACTGTGTGAAGCTTTAAAGGAACC 2845

Qy       2829 ATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGA 2888
Db       2846 TACTTGTTACCTTCAAGAACTGGAACTAGTGGACTGCCAACTCACACAGAACTGCTGCGA 2905

Qy       2889 GAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAA 2948
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Qy       2949 TGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGT 3008
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Qy       3009 TCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTC 3068
Db       3026 CCTGAGGAGACTTGGGTTGGGGGCATGTAAGTTGACTTCCAATTGCTGTGAGGCATTGTC 3085

Qy       3069 CTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAG 3128
Db       3086 ATTGGCCATCTCTTGCAACCCTCACCTGAACAGCCTAAACCTGGTGAAGAATGACTTCAG 3145

Qy       3129 TCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGAT 3188

Db       3146 TACATCGGGGATGTTGAAGCTGTGCTCTGCGTTCCAATGCCCTGTCTCTAACCTGGGGAT 3205

Qy       3189 AATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCA 3248
Db       3206 AATTGGCCTGTGGAAGCAGGAGTACTATGCCCGAGTGAGAAGACAGCTGGAGGAAGTTGA 3265

Qy       3249 GCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 3308
Db       3266 GTTTGTCAAGCCCCACGTGGTGATTGATGGTGATTGGTATGCTAGTGATGAAGATGACCG 3325

Qy       3309 ACAC 3312
Db       3326 AAAC 3329
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RESULT 15
ABK48609
ID ABK48609 standard; cDNA; 1157 BP.
XX
AC ABK48609;
XX
DT 13-AUG-2002 (first entry)
XX
DE Human MATER cDNA fragment #1.
XX
KW Human; gene; ss; contraceptive; antiinfertility; MATER;
KW Maternal antigen that embryos require; MATER null phenotype; oocyte;
KW early embryonic survival; premature ovarian failure; POF;
KW autoimmune infertility; chromosome 19; gene therapy; fertility.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .1155
FT   /*tag= a
FT   /product= "Human MATER"
FT   /partial
FT   /note= "No start or stop codon shown"
XX
PN WO200232955-A1.
XX
PD 25-APR-2002.
XX
PF 04-APR-2001; 2001WO-US010981.
XX
PR 18-OCT-2000; 2000US-0241510P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nelson LM, Tong Z;
XX
DR WPI; 2002-454595/48.
DR P-PSDB; AAU79523.
XX
PT New isolated human Maternal Antigen That Embryos Require protein and
PT polynucleotide, useful in diagnosing or treating fertility or reduced
PT fertility, or as a contraceptive.
XX
PS Claim 11; Page 68-69; 93pp; English.
XX
CC The invention discloses an isolated human MATER (Maternal Antigen That
CC Embryos Require) protein, which can complement a MATER null phenotype in
CC which zygotes arising from the oocyte do not progress beyond the two-cell
CC stage. MATER is required for early embryonic survival and abnormal levels
CC of the protein can lead to premature ovarian failure (POF) and can be
CC caused by under or over expression of MATER or an autoimmune response to
CC MATER. MATER is a single-copy Maternal effect gene found on chromosome
CC 19. The MATER protein and polynucleotide, by gene therapy, are useful in
CC diagnosing or treating fertility and reduced fertility. In particular,
CC the MATER protein is useful as a contraceptive agent, or for influencing
CC (either inhibiting or enhancing) fertility and can be used to detect a
CC predisposition to infertility or reduced fertility, or for presymptomatic

CC screening of an individual for infertility/reduced fertility. The protein
CC and polynucleotide are also useful for detecting an excess or deficiency,
CC or genetic mutation, of the MATER protein in a mammalian subject (e.g. a
CC human or a mouse) or for screening for a compound useful in influencing
CC MATER-mediated fertility. The sequence presented is the human MATER cDNA
CC fragment #1, which was isolated from a human cDNA library
XX
SQ Sequence 1157 BP; 240 A; 324 C; 320 G; 273 T; 0 U; 0 Other;

Query Match 28.6%; Score 1152.8; DB 6; Length 1157;
Best Local Similarity 99.8%; Pred. No. 9.3e-308;
Matches 1154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        754 CAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 813
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CAAGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 60

Qy        814 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 120

Qy        874 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 180

Qy        934 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 240

Qy        994 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 1053
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Db        241 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 300

Qy       1054 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 1113
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Db        301 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 360

Qy       1114 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 420

Qy       1174 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 480

Qy       1234 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 1293
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Db        481 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 540

Qy       1294 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 600

Qy       1354 TCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 1413
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Qy       1414 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 1473
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Qy       1474 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 1533
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Qy       1534 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 1593
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Qy       1594 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 1653
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Qy       1714 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1773
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Qy       1774 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1833
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Qy       1834 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1893
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Qy       1894 TCCTTCTGCCTCCAGC 1909
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Job time : 2052 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	221.4	5.5	4556	4	US-09-388-221B-9	Sequence 9, Appli
	3	220.6	5.5	4200	4	US-09-388-221B-3	Sequence 3, Appli
	4	220.6	5.5	4332	4	US-09-388-221B-5	Sequence 5, Appli
	5	220.6	5.5	4466	4	US-09-388-221B-11	Sequence 11, Appl
	6	183.8	4.6	1371	2	US-08-910-731-1	Sequence 1, Appli
	7	183.8	4.6	1371	2	US-08-795-395-1	Sequence 1, Appli
	8	182.4	4.5	1386	2	US-08-910-731-5	Sequence 5, Appli
	9	180.8	4.5	1371	2	US-08-910-731-7	Sequence 7, Appli
	10	175.8	4.4	1374	2	US-08-910-731-3	Sequence 3, Appli
	11	175.8	4.4	1374	2	US-08-795-395-3	Sequence 3, Appli
c	12	61	1.5	7218	1	US-08-232-463-14	Sequence 14, Appl
	13	60	1.5	376	4	US-09-023-655-395	Sequence 395, App
	14	51.4	1.3	298336	4	US-09-949-016-16600	Sequence 16600, A
c	15	50.8	1.3	64309	4	US-09-949-016-14581	Sequence 14581, A
	16	47.4	1.2	4485	4	US-09-949-016-3209	Sequence 3209, Ap
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	18	47.4	1.2	4486	4	US-10-014-269-33	Sequence 33, Appl
	19	46.6	1.2	1276	3	US-09-177-325-2	Sequence 2, Appli
	20	46.6	1.2	1276	3	US-09-411-812A-2	Sequence 2, Appli
	21	46.6	1.2	1276	3	US-09-590-113-2	Sequence 2, Appli
	22	46.4	1.1	2780	4	US-09-620-312D-358	Sequence 358, App
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	27	43.2	1.1	193303	4	US-09-497-855A-44	Sequence 44, Appl
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	29	42.8	1.1	767677	4	US-09-949-016-12147	Sequence 12147, A
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	32	42.6	1.1	1005	4	US-09-252-991A-10976	Sequence 10976, A
c	33	42.6	1.1	1185	4	US-09-252-991A-11203	Sequence 11203, A
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	37	42	1.0	3117	4	US-09-614-221A-275	Sequence 275, App
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c	41	41.2	1.0	810	4	US-09-614-221A-103	Sequence 103, App
	42	41.2	1.0	43795	3	US-08-742-185-101	Sequence 101, App
	43	41	1.0	505	4	US-09-621-976-15639	Sequence 15639, A
c	44	41	1.0	10391	4	US-09-902-540-958	Sequence 958, App
	45	40.4	1.0	240157	4	US-09-949-016-16264	Sequence 16264, A

ALIGNMENTS

RESULT 1
US-09-388-221B-1
; Sequence 1, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4422)
US-09-388-221B-1

Query Match 5.5%; Score 221.4; DB 4; Length 4422;
Best Local Similarity 47.9%; Pred. No. 9.1e-55;
Matches 953; Conservative 0; Mismatches 966; Indels 72; Gaps 8;

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Qy        532 TTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGA 591
              ||||   ||| || |     |       |||||||  ||  | ||||| ||       | |||
Db        952 TTTGGCCCAGGCCTGGATACCCAAGAACCTCGCATAGTCATACTGCAGGGGGCTGCTGGA 1011

Qy        592 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 651
              |||||||| ||  | || |||||    | |    |      |||||  |  |||    || ||
Db       1012 ATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGGAGAGGCCAGCTGTAT 1071

Qy        652 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 711
                ||     |||     | |||||||  | ||  |   ||||| ||    | |   |||| |
Db       1072 GGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTGGCCCAGTCCAAGGTG 1131

Qy        712 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 771
                ||| || | ||| |||||    |  ||  || ||| | | | ||||||  | |   ||
Db       1132 GTGAGTCTCGCTGAGCTCATCGGAAAAGATGGGACAGCCACTCCGGCTCCCATTAGACAG 1191

Qy        772 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 831
              ||| ||||  | |||||  |||||  | ||||||  | ||  ||| | |||||  |  || |
Db       1192 ATCCTGTCTAGGCCAGAGCGGCTGCTCTTCATCCTCGATGGTGTAGATGAGCCAGGATGG 1251

Qy        832 GTCCTCAACAATGACA---CAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTC 888
              ||| |  |  |    |   | |||||||     |||||    ||  |||||  ||
Db       1252 GTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAGCCACAGCCGGCGGAT 1311

Qy        889 ACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACC 948
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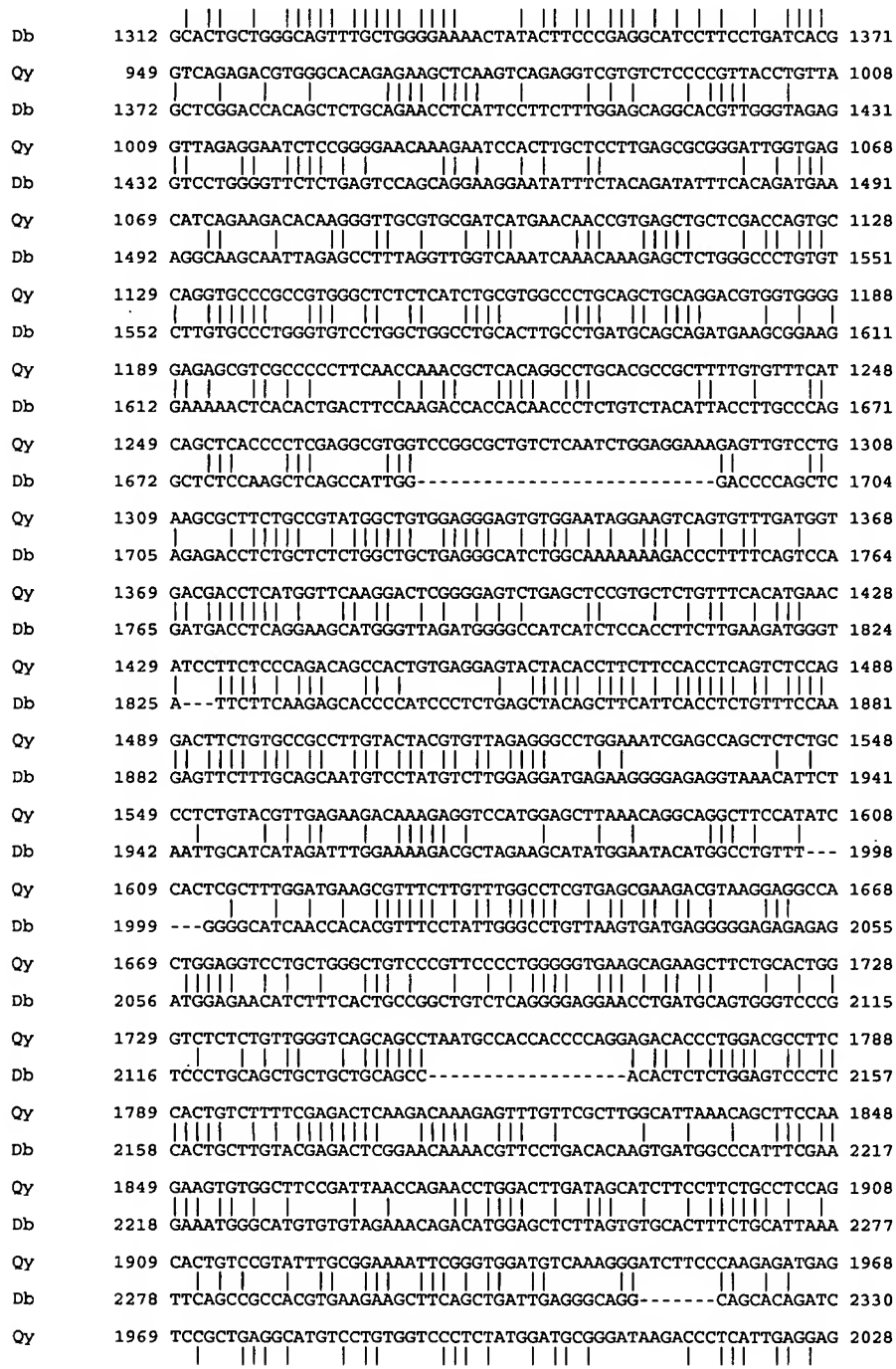
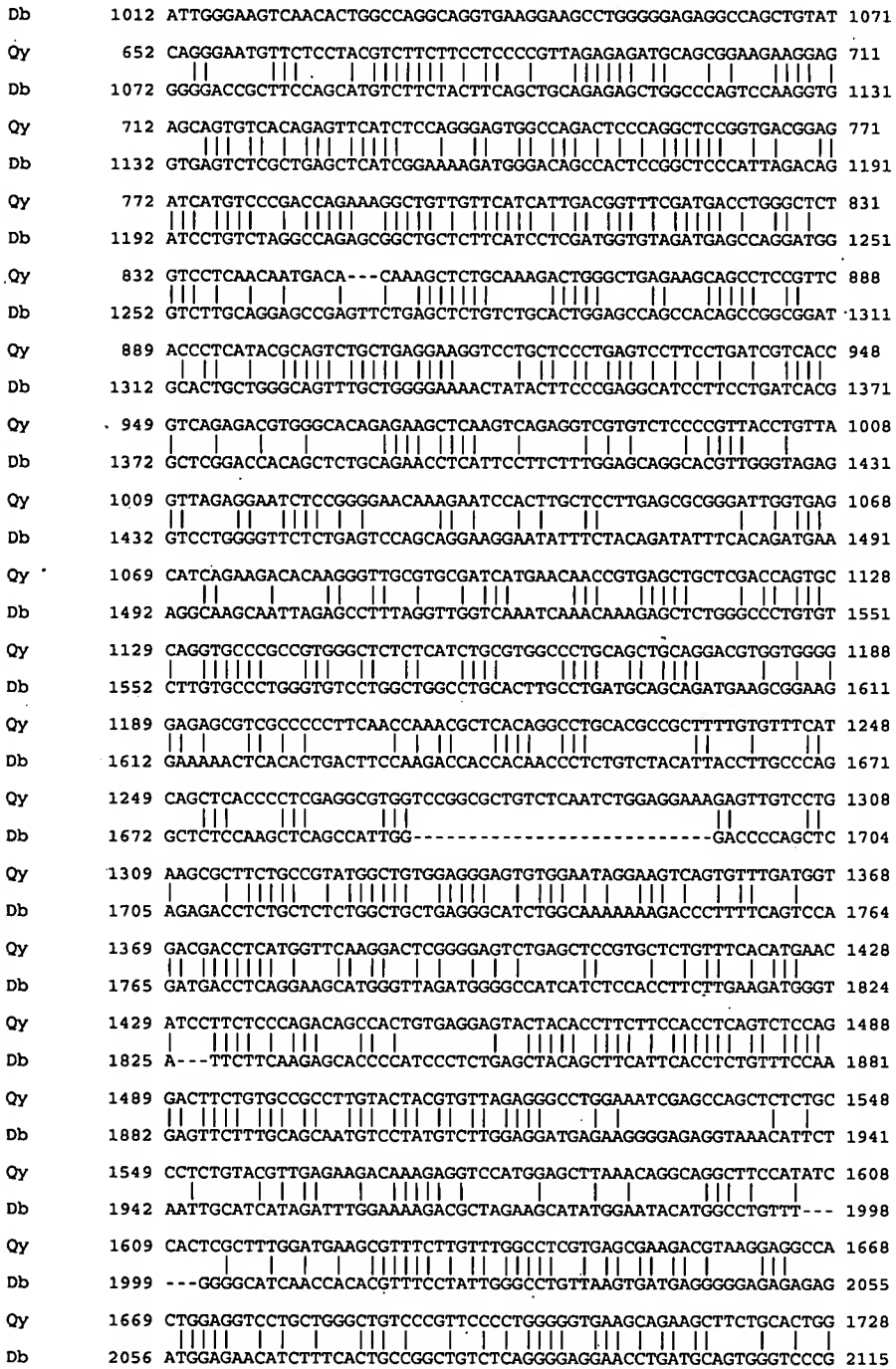


RESULT 2
US-09-388-221B-9
; Sequence 9, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 4556
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4365)
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-09-388-221B-9

Query Match 5.5%; Score 221.4; DB 4; Length 4556;
Best Local Similarity 47.9%; Pred. No. 9.3e-55;
Matches 953; Conservative 0; Mismatches 966; Indels 72; Gaps 8;



RESULT 3
US-09-388-221B-3
; Sequence 3, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4200
; TYPE: DNA

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;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(4197)
US-09-388-221B-3

  Query Match             5.5%;  Score 220.6;  DB 4;  Length 4200;
  Best Local Similarity   48.0%;  Pred. No. 1.5e-54;
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Db        952 TTTGGCCCAGGCCTGGATACCCAAGAACCTCGCATAGTCATACTGCAGGGGGCTGCTGGA 1011

Qy        592 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 651
              |||||||| ||  | || |||||   | |    |      |||||  |  |||    || ||
Db       1012 ATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGGAGAGGCCAGCTGTAT 1071

Qy        652 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 711
              ||      |||    | |||||||| | ||  |   ||||||| ||    | |   |||| |
Db       1072 GGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTGGCCCAGTCCAAGGTG 1131

Qy        712 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 771
              |||  || | |||  |||||    |  ||  || ||| | | | ||||||  | |   ||
Db       1132 GTGAGTCTCGCTGAGCTCATCGGAAAAGATGGGACAGCCACTCCGGCTCCCATTAGACAG 1191

Qy        772 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 831
              |||  ||||  | |||||  |||||  | ||||||  | ||  |||  | |||||  |   || |
Db       1192 ATCCTGTCTAGGCCAGAGCGGCTGCTCTTCATCCTCGATGGTGTAGATGAGCCAGGATGG 1251

Qy        832 GTCCTCAACAATGACA---CAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTC 888
              |||  |   |    |   |  |  |||||||     |||||    ||   |||||  ||
Db       1252 GTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAGCCACAGCCGGCGGAT 1311

Qy        889 ACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACC 948
              | ||  |  ||||| |||||  ||||      | ||  || |||  | | |  |  ||||
Db       1312 GCACTGCTGGGCAGTTTGCTGGGGAAAACTATACTTCCCGAGGCATCCTTCCTGATCACG 1371

Qy        949 GTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTA 1008
              |   |   |   |    |||| ||||   |     | | |    | ||||    |
Db       1372 GCTCGGACCACAGCTCTGCAGAACCTCATTCCTTCTTTGGAGCAGGCACGTTGGGTAGAG 1431

Qy       1009 GTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAG 1068
              ||     ||  |||| | |       || |   | |   ||          | | |||
Db       1432 GTCCTGGGGTTCTCTGAGTCCAGCAGGAAGGAATATTTCTACAGATATTTCACAGATGAA 1491

Qy       1069 CATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGC 1128
              ||    |    ||  ||  |   | |||      |||   |||||     | || |||
Db       1492 AGGCAAGCAATTAGAGCCTTTAGGTTGGTCAAATCAAACAAAGAGCTCTGGGCCCTGTGT 1551

Qy       1129 CAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGG 1188
              |  ||||||   |||  ||  ||   ||||    ||||  || ||||      |  | |
Db       1552 CTTGTGCCCTGGGTGTCCTGGCTGGCCTGCACTTGCCTGATGCAGCAGATGAAGCGGAAG 1611

Qy       1189 GAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCAT 1248
              || |   || | |       | | ||   ||||  |||       ||    |    ||
Db       1612 GAAAAACTCACACTGACTTCCAAGACCACCACAACCCTCTGTCTACATTACCTTGCCCAG 1671

Qy       1249 CAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTG 1308
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Db       1672 GCTCTCCAAGCTCAGCCATTGG--------------------------GACCCCAGCTC 1704

Qy       1309 AAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGT 1368
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Db       1705 AGAGACCTCTGCTCTCTGGCTGCTGAGGGCATCTGGCAAAAAAAGACCCTTTTCAGTCCA 1764

Qy       1369 GACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAAC 1428
              || |||||||  |   || ||  | |  | | |      ||     |  | ||  | |||
Db       1765 GATGACCTCAGGAAGCATGGGTTAGATGGGGCCATCATCTCCACCTTCTTGAAGATGGGT 1824

Qy       1429 ATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAG 1488
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Db       1825 A---TTCTTCAAGAGCACCCCATCCCTCTGAGCTACAGCTTCATTCACCTCTGTTTCCAA 1881

Qy       1489 GACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGC 1548
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Db       1882 GAGTTCTTTGCAGCAATGTCCTATGTCTTGGAGGATGAGAAGGGGAGAGGTAAACATTCT 1941

Qy       1549 CCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATC 1608
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Db       1942 AATTGCATCATAGATTTGGAAAAGACGCTAGAAGCATATGGAATACATGGCCTGTTTGGG 2001

Qy       1609 CACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCA 1668
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Db       2002 GCATC------AACCACACGTTTCCTATTGGGCCTGTTAAGTGATGAGGGGGAGAGAGAG 2055

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Db       2056 ATGGAGAACATCTTTCACTGCCGGCTGTCTCAGGGGAGGAACCTGATGCAGTGGGTCCCG 2115

Qy       1729 GTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTC 1788
                |  | | ||  | ||||||                  | || | |||||  || ||
Db       2116 TCCCTGCAGCTGCTGCTGCAGCC------------------ACACTCTCTGGAGTCCCTC 2157

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Db       2158 CACTGCTTGTACGAGACTCGGAACAAAACGTTCCTGACACAAGTGATGGCCCATTTCGAA 2217

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Qy       1969 TCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAG 2028
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Db       2331 AACATGGAGCCCCACCATGGTAGTCCTGTTCAGGTGGG-----TCCCAGTCACAGATGCC 2385

Qy       2029 CAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTG 2088
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Db       2386 TATTGGCAGATTCTCTTCTCCGTCCTCAAGGTCACCAGAAACCTGAAGGAGCTGGACCTA 2445

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Db       2566 GACCTTGCCTTTGGGCTGAGAGCCAACCAGACCCTGACCGAGCTGGACCTGAGCTTCAAT 2625

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Db       2626 GTGCTCACGGATGCTGGAGCCAAACACCTTTGCCAGAGACTGAGACAGCCGAGCTGCAAG 2685

Qy       2326 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2385
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Db       2686 CTACAGCGACTGCAGCTGGTCAGCTGTGGCCTCACGTCTGACTGCTGCCAGGACCTGGCC 2745

Qy       2386 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2445
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RESULT 4
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; Sequence 5, Application US/09388221B
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; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 4332
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4332)
US-09-388-221B-5

Query Match 5.5%; Score 220.6; DB 4; Length 4332;
Best Local Similarity 48.0%; Pred. No. 1.6e-54;
Matches 939; Conservative 0; Mismatches 944; Indels 72; Gaps 8;

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Db        952 TTTGGCCCAGGCCTGGATACCCAAGAACCTCGCATAGTCATACTGCAGGGGGCTGCTGGA 1011

Qy        592 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 651
              ||||||||  ||   | ||  |||||    | |    |      |||||  |  |||     || ||
Db       1012 ATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGGAGAGGCCAGCTGTAT 1071

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Db       1072 GGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTGGCCCAGTCCAAGGTG 1131

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Db       1252 GTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAGCCACAGCCGGCGGAT 1311

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              | ||  |  ||||| ||||| ||||      | || || ||| | | |  |  ||||
Db       1312 GCACTGCTGGGCAGTTTGCTGGGGAAAACTATACTTCCCGAGGCATCCTTCCTGATCACG 1371

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              |   |   |   |      |||| ||||   |      | | |    | ||||   |
Db       1372 GCTCGGACCACAGCTCTGCAGAACCTCATTCCTTCTTTGGAGCAGGCACGTTGGGTAGAG 1431

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Db       1432 GTCCTGGGGTTCTCTGAGTCCAGCAGGAAGGAATATTTCTACAGATATTTCACAGATGAA 1491

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Db       1552 CTTGTGCCCTGGGTGTCCTGGCTGGCCTGCACTTGCCTGATGCAGCAGATGAAGCGGAAG 1611

Qy       1189 GAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCAT 1248
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Db       1612 GAAAAACTCACACTGACTTCCAAGACCACCACAACCCTCTGTCTACATTACCTTGCCCAG 1671

Qy       1249 CAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTG 1308
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Db       1672 GCTCTCCAAGCTCAGCCATTGG--------------------------GACCCCAGCTC 1704

Qy       1309 AAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGT 1368
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Db       1705 AGAGACCTCTGCTCTCTGGCTGCTGAGGGCATCTGGCAAAAAAAGACCCTTTTCAGTCCA 1764

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Db       1765 GATGACCTCAGGAAGCATGGGTTAGATGGGGCCATCATCTCCACCTTCTTGAAGATGGGT 1824

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              || |||| ||| ||  ||| ||| || || ||||    | |             | |
Db       1882 GAGTTCTTTGCAGCAATGTCCTATGTCTTGGAGGATGAGAAGGGGAGAGGTAAACATTCT 1941

Qy       1549 CCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATC 1608
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Db       1942 AATTGCATCATAGATTTGGAAAAGACGCTAGAAGCATATGGAATACATGGCCTGTTTGGG 2001

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Db       2002 GCATC------AACCACACGTTTCCTATTGGGCCTGTTAAGTGATGAGGGGGAGAGAGAG 2055

Qy       1669 CTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGG 1728
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Db       2056 ATGGAGAACATCTTTCACTGCCGGCTGTCTCAGGGGAGGAACCTGATGCAGTGGGTCCCG 2115

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Db       2158 CACTGCTTGTACGAGACTCGGAACAAAACGTTCCTGACACAAGTGATGGCCCATTTCGAA 2217

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              ||| || |  |     |  |     || |||| |  |||  |  | ||||||  |  |
Db       2218 GAAATGGGCATGTGTGTAGAAACAGACATGGAGCTCTTAGTGTGCACTTTCTGCATTAAA 2277

Qy       1909 CACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAG 1968
              | | |  |  ||  |||  |||  | ||  ||  ||      ||  | |
Db       2278 TTCAGCCGCCACGTGAAGAAGCTTCAGCTGATTGAGGGCAGG-------CAGCACAGATC 2330

Qy       1969 TCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAG 2028
              |  ||| |   | ||     ||| |   | ||. |       |  ||| || |
Db       2331 AACATGGAGCCCCACCATGGTAGTCCTGTTCAGGTGGG-----TCCCAGTCACAGATGCC 2385

Qy       2029 CAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTG 2088
              | ||| |   | ||| |||| | ||      |  | |||||  | ||||||||||
Db       2386 TATTGGCAGATTCTCTTCTCCGTCCTCAAGGTCACCAGAAACCTGAAGGAGCTGGACCTA 2445

Qy       2089 GGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCC 2148
              |  | | |  |||    |  || |||||  || |||   | |||| |  ||
Db       2446 AGTGGAAACTCGCTGAGCCACTCTGCAGTGAAGAGTCTTTGTAAGACCCTGAGACGCCCT 2505

Qy       2149 ACCTGCAAGATACAGACCCTGATGTT---TAGAAATGCACAGATTACCCCTGGTGTGCAG 2205
              ||||   |  |||||||| |||  | |  || |  |  |  |  |  ||
Db       2506 CGCTGCCTCCTGGAGACCCTGCGGTTGGCTGGCTGTGGCCTCACAGCTGAGGACTGCAAG 2565

Qy       2206 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2265
              ||||          | |  |||||||  | ||| |      ||  || || |   ||
Db       2566 GACCTTGCCTTTGGGCTGAGAGCCAACCAGACCCTGACCGAGCTGGACCTGAGCTTCAAT 2625

Qy       2266 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2325
              || | ||| |  |  |  |          || |     | | ||| || |  ||   |
Db       2626 GTGCTCACGGATGCTGGAGCCAAACACCTTTGCCAGAGACTGAGACAGCCGAGCTGCAAG 2685

Qy       2326 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2385
              |  ||   ||  |||||  |||||||  | ||   || ||| | || | |  | ||
Db       2686 CTACAGCGACTGCAGCTGGTCAGCTGTGGCCTCACGTCTGACTGCTGCCAGGACCTGGCC 2745
```

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Qy       2386 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2445
Db       2746 TCTGTGCTTAGTGCCAGCCCCAGCCTGAAGGAGCTAGACCTGCAGCAGAACAACCTGGAT 2805

Qy       2446 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAG 2480
Db       2806 GACGTTGGCGTGCGACTGCTCTGTGAGGGGCTCAG 2840


RESULT 5
US-09-388-221B-11
; Sequence 11, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 4466
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(4272)
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Construct
US-09-388-221B-11

  Query Match             5.5%;  Score 220.6;  DB 4;  Length 4466;
  Best Local Similarity   48.0%;  Pred. No. 1.6e-54;
  Matches  939;  Conservative    0;  Mismatches  944;  Indels   72;  Gaps    8;

Qy        532 TTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGA 591
Db        952 TTTGGCCCAGGCCTGGATACCCAAGAACCTCGCATAGTCATACTGCAGGGGGCTGCTGGA 1011

Qy        592 ATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTAC 651
Db       1012 ATTGGGAAGTCAACACTGGCCAGGCAGGTGAAGGAAGCCTGGGGGAGAGGCCAGCTGTAT 1071

Qy        652 CAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAG 711
Db       1072 GGGGACCGCTTCCAGCATGTCTTCTACTTCAGCTGCAGAGAGCTGGCCCAGTCCAAGGTG 1131

Qy        712 AGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAG 771
Db       1132 GTGAGTCTCGCTGAGCTCATCGGAAAAGATGGGACAGCCACTCCGGCTCCCATTAGACAG 1191

Qy        772 ATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCT 831
Db       1192 ATCCTGTCTAGGCCAGAGCGGCTGCTCTTCATCCTCGATGGTGTAGATGAGCCAGGATGG 1251

Qy        832 GTCCTCAACAATGACA---CAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTC 888
Db       1252 GTCTTGCAGGAGCCGAGTTCTGAGCTCTGTCTGCACTGGAGCCAGCCACAGCCGGCGGAT 1311

Qy        889 ACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACC 948
Db       1312 GCACTGCTGGGCAGTTTGCTGGGGAAAACTATACTTCCCGAGGCATCCTTCCTGATCACG 1371

Qy        949 GTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTA 1008
Db       1372 GCTCGGACCACAGCTCTGCAGAACCTCATTCCTTCTTTGGAGCAGGCACGTTGGGTAGAG 1431

Qy       1009 GTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAG 1068
Db       1432 GTCCTGGGGTTCTCTGAGTCCAGCAGGAAGGAATATTTCTACAGATATTTCACAGATGAA 1491

Qy       1069 CATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGC 1128
Db       1492 AGGCAAGCAATTAGAGCCTTTAGGTTGGTCAAATCAAACAAAGAGCTCTGGGCCCTGTGT 1551

Qy       1129 CAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGG 1188
Db       1552 CTTGTGCCCTGGGTGTCCTGGCTGGCCTGCACTTGCCTGATGCAGCAGATGAAGCGGAAG 1611

Qy       1189 GAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCAT 1248
Db       1612 GAAAAACTCACACTGACTTCCAAGACCACCACAACCCTCTGTCTACATTACCTTGCCCAG 1671

Qy       1249 CAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTG 1308
Db       1672 GCTCTCCAAGCTCAGCCATTGG----------------------------GACCCCAGCTC 1704

Qy       1309 AAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGT 1368
Db       1705 AGAGACCTCTGCTCTCTGGCTGCTGAGGGCATCTGGCAAAAAAAGACCCTTTTCAGTCCA 1764

Qy       1369 GACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAAC 1428
Db       1765 GATGACCTCAGGAAGCATGGGTTAGATGGGGCCATCATCTCCACCTTCTTGAAGATGGGT 1824

Qy       1429 ATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAG 1488
Db       1825 A---TTCTTCAAGAGCACCCCATCCCTCTGAGCTACAGCTTCATTCACCTCTGTTTCCAA 1881

Qy       1489 GACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGC 1548
Db       1882 GAGTTCTTTGCAGCAATGTCCTATGTCTTGGAGGATGAGAAGGGGAGAGGTAAACATTCT 1941

Qy       1549 CCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATC 1608
Db       1942 AATTGCATCATAGATTTGGAAAAGACGCTAGAAGCATATGGAATACATGGCCTGTTTGGG 2001

Qy       1609 CACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCA 1668
Db       2002 GCATC------AACCACACGTTTCCTATTGGGCCTGTTAAGTGATGAGGGGGAGAGAGAG 2055

Qy       1669 CTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGG 1728
Db       2056 ATGGAGAACATCTTTCACTGCCGGCTGTCTCAGGGGAGGAACCTGATGCAGTGGGTCCCG 2115

Qy       1729 GTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTC 1788
Db       2116 TCCCTGCAGCTGCTGCTGCAGCC----------------ACACTCTCTGGAGTCCCTC 2157

Qy       1789 CACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAA 1848
Db       2158 CACTGCTTGTACGAGACTCGGAACAAAACGTTCCTGACACAAGTGATGGCCCATTTCGAA 2217

Qy       1849 GAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAG 1908
Db       2218 GAAATGGGCATGTGTGTAGAAACAGACATGGAGCTCTTAGTGTGCACTTTCTGCATTAAA 2277

Qy       1909 CACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAG 1968
Db       2278 TTCAGCCGCCACGTGAAGAAGCTTCAGCTGATTGAGGGCAGG-------CAGCACAGATC 2330

Qy       1969 TCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAG 2028
Db       2331 AACATGGAGCCCCACCATGGTAGTCCTGTTCAGGTGGG-----TCCCAGTCACAGATGCC 2385

Qy       2029 CAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTG 2088
Db       2386 TATTGGCAGATTCTCTTCTCCGTCCTCAAGGTCACCAGAAACCTGAAGGAGCTGGACCTA 2445

Qy       2089 GGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCC 2148
Db       2446 AGTGGAAACTCGCTGAGCCACTCTGCAGTGAAGAGTCTTTGTAAGACCCTGAGACGCCCT 2505

Qy       2149 ACCTGCAAGATACAGACCCTGATGTT---TAGAAATGCACAGATTACCCCTGGTGTGCAG 2205
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Db       2506 CGCTGCCTCCTGGAGACCCTGCGGTTGGCTGGCTGTGGCCTCACAGCTGAGGACTGCAAG 2565

Qy       2206 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2265

Db       2566 GACCTTGCCTTTGGGCTGAGAGCCAACCAGACCCTGACCGAGCTGGACCTGAGCTTCAAT 2625

Qy       2266 CACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTG 2325

Db       2626 GTGCTCACGGATGCTGGAGCCAAACACCTTTGCCAGAGACTGAGACAGCCGAGCTGCAAG 2685

Qy       2326 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2385

Db       2686 CTACAGCGACTGCAGCTGGTCAGCTGTGGCCTCACGTCTGACTGCTGCCAGGACCTGGCC 2745

Qy       2386 CAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACA 2445

Db       2746 TCTGTGCTTAGTGCCAGCCCCAGCCTGAAGGAGCTAGACCTGCAGCAGAACAACCTGGAT 2805

Qy       2446 GACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAG 2480

Db       2806 GACGTTGGCGTGCGACTGCTCTGTGAGGGGCTCAG 2840


RESULT 6
US-08-910-731-1
; Sequence 1, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-910-731-1

  Query Match             4.6%;  Score 183.8;  DB 2;  Length 1371;
  Best Local Similarity   47.2%;  Pred. No. 7e-44;
  Matches  591;  Conservative    0;  Mismatches  657;  Indels    3;  Gaps    1;

Qy       2016 CCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCG 2075

Db        102 CCTCACGGAGGAGCACTGCAAGGACATCGGTTCTGCCCTCCGGGCCAACCCCTCCCTGAC 161

Qy       2076 GCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAA 2135

Db        162 CGAGCTCTGCCTCCGCACCAACGAGCTGGGCGATGCCGGCGTGCACCTGGTGCTGCAGGG 221

Qy       2136 GCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCC- 2194

Db        222 CCTGCAGAGCCCCACCTGCAAGATCCAGAAGCTCAGCCTGCAGAACTGCTCCCTGACCGA 281

Qy       2195 --CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAA 2252

Db        282 GGCGGGCTGCGGGGTCCTGCCCAGCACGCTGCGCTCCCTGCCCACGCTGCGGGAGCTGCA 341

Qy       2253 CTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACA 2312

Db        342 TCTCAGCGACAACCCACTGGGGGACGCCGGCCTGCGGCTGCTCTGTGAGGGGCTCCTGGA 401

Qy       2313 CCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTA 2372

Db        402 CCCCCAGTGCCACCTGGAGAAGCTGCAGTTGGAGTACTGCCGCCTGACGGCCGCCAGCTG 461

Qy       2373 CCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGG 2432

Db        462 CGAGCCCCTGGCCTCGGTGCTCAGGGCCACGCGGGCCTTGAAGGAGCTCACGGTGAGCAA 521

Qy       2433 AAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTG 2492

Db        522 CAACGACATCGGCGAGGCCGGCGCCCGGGTGCTGGGCCAGGGTCTGGCAGACTCTGCCTG 581

Qy       2493 CGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCT 2552

Db        582 CCAGCTGGAGACGCTCAGGCTGGAGAACTGCGGTCTCACGCCAGCCAACTGCAAAGACCT 641

Qy       2553 GGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCT 2612

Db        642 GTGCGGAATTGTGGCCTCCCAGGCCTCGCTGAGGGAGCTTGACCTGGGCAGCAACGGGCT 701

Qy       2613 GGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCA 2672

Db        702 GGGCGACGCGGGCATAGCCGAGCTGTGCCCCGGGCTCTTGAGCCCCGCCTCCCGCCTCAA 761

Qy       2673 GAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGC 2732

Db        762 GACCCTGTGGCTCTGGGAGTGTGACATCACCGCCAGTGGCTGCAGAGACCTCTGCCGTGT 821

Qy       2733 GCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAA 2792

Db        822 CCTCCAGGCCAAGGAGACCCTGAAGGAGCTCAGTCTGGCGGGCAACAAGCTGGGCGACGA 881

Qy       2793 TGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGA 2852

Db        882 GGGCGCCCGGCTGCTGTGCGAGAGCCTGCTGCAGCCCGGCTGCCAGCTGGAGTCCCTGTG 941

Qy       2853 GTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAG 2912

Db        942 GGTGAAGTCCTGCAGCCTCACGGCGGCCTGCTGCCAGCACGTCAGCTTGATGCTGACCCA 1001

Qy       2913 GAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGC 2972

Db       1002 GAACAAGCATCTCCTGGAACTTCAGTTGAGCAGCAACAAGCTGGGTGACTCTGGCATCCA 1061

Qy       2973 TGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGC 3032
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Db       1062 GGAGCTGTGCCAGGCCCTGAGCCAGCCGGGCACCACACTGCGGGTGCTCTGTCTTGGGGA 1121

Qy       3033 ATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCA 3092

Db       1122 CTGTGAGGTGACCAACAGCGGCTGCAGCAGCCTCGCCTCGCTCCTGCTGGCCAACCGCAG 1181

Qy       3093 TCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTG 3152

Db       1182 CCTGCGAGAGCTGGACCTGAGCAACAACTGTGTGGGCGACCCGGGCGTCCTGCAGCTGCT 1241

Qy       3153 TTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTA 3212

Db       1242 GGGGAGCCTGGAGCAGCCGGGCTGCGCCCTGGAGCAGCTGGTCCTGTACGACACCTACTG 1301

Qy       3213 CCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCG 3263

Db       1302 GACGGAGGAGGTGGAGGACCGCCTGCAGGCCCTGGAGGGGAGCAAGCCCGG 1352


RESULT 7
US-08-795-395-1
; Sequence 1, Application US/08795395
; Patent No. 5965399
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Cloning and Expression of Rat Liver and
;    TITLE OF INVENTION:  Porcine Liver Ribonuclease Inhibitor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,395
;      FILING DATE:  04-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-795-395-1

  Query Match             4.6%;  Score 183.8;  DB 2;  Length 1371;
  Best Local Similarity   47.2%;  Pred. No. 7e-44;
  Matches  591;  Conservative    0;  Mismatches  657;  Indels    3;  Gaps    1;

Qy       2016 CCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCG 2075

Db        102 CCTCACGGAGGAGCACTGCAAGGACATCGGTTCTGCCCTCCGGGCCAACCCCTCCCTGAC 161

Qy       2076 GCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAA 2135

Db        162 CGAGCTCTGCCTCCGCACCAACGAGCTGGGCGATGCCGGCGTGCACCTGGTGCTGCAGGG 221

Qy       2136 GCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCC- 2194

Db        222 CCTGCAGAGCCCCACCTGCAAGATCCAGAAGCTCAGCCTGCAGAACTGCTCCCTGACCGA 281

Qy       2195 --CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAA 2252

Db        282 GGCGGGCTGCGGGGTCCTGCCCAGCACGCTGCGCTCCCTGCCCACGCTGCGGGAGCTGCA 341

Qy       2253 CTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACA 2312

Db        342 TCTCAGCGACAACCCACTGGGGGACGCCGGCCTGCGGCTGCTCTGTGAGGGGCTCCTGGA 401

Qy       2313 CCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTA 2372

Db        402 CCCCCAGTGCCACCTGGAGAAGCTGCAGTTGGAGTACTGCCGCCTGACGGCCGCCAGCTG 461

Qy       2373 CCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGG 2432

Db        462 CGAGCCCCTGGCCTCGGTGCTCAGGGCCACGCGGGCCTTGAAGGAGCTCACGGTGAGCAA 521

Qy       2433 AAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTG 2492

Db        522 CAACGACATCGGCGAGGCCGGCGCCCGGGTGCTGGGCCAGGGTCTGGCAGACTCTGCCTG 581

Qy       2493 CGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCT 2552

Db        582 CCAGCTGGAGACGCTCAGGCTGGAGAACTGCGGTCTCACGCCAGCCAACTGCAAAGACCT 641

Qy       2553 GGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCT 2612

Db        642 GTGCGGAATTGTGGCCTCCCAGGCCTCGCTGAGGGAGCTTGACCTGGGCAGCAACGGGCT 701

Qy       2613 GGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCA 2672

Db        702 GGGCGACGCGGGCATAGCCGAGCTGTGCCCCGGGCTCTTGAGCCCCGCCTCCCGCCTCAA 761

Qy       2673 GAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGC 2732

Db        762 GACCCTGTGGCTCTGGGAGTGTGACATCACCGCCAGTGGCTGCAGAGACCTCTGCCGTGT 821

Qy       2733 GCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAA 2792

Db        822 CCTCCAGGCCAAGGAGACCCTGAAGGAGCTCAGTCTGGCGGGCAACAAGCTGGGCGACGA 881

Qy       2793 TGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGA 2852

Db        882 GGGCGCCCGGCTGCTGTGCGAGAGCCTGCTGCAGCCCGGCTGCCAGCTGGAGTCCCTGTG 941

Qy       2853 GTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAG 2912

Db        942 GGTGAAGTCCTGCAGCCTCACGGCGGCCTGCTGCCAGCACGTCAGCTTGATGCTGACCCA 1001

Qy       2913 GAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGC 2972

Db       1002 GAACAAGCATCTCCTGGAACTTCAGTTGAGCAGCAACAAGCTGGGTGACTCTGGCATCCA 1061

Qy       2973 TGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGC 3032

Db       1062 GGAGCTGTGCCAGGCCCTGAGCCAGCCGGGCACCACACTGCGGGTGCTCTGTCTTGGGGA 1121

Qy       3033 ATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCA 3092

Db       1122 CTGTGAGGTGACCAACAGCGGCTGCAGCAGCCTCGCCTCGCTCCTGCTGGCCAACCGCAG 1181

Qy       3093 TCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTG 3152
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Db       1182 CCTGCGAGAGCTGGACCTGAGCAACAACTGTGTGGGCGACCCGGGCGTCCTGCAGCTGCT 1241

Qy       3153 TTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTA 3212

Db       1242 GGGGAGCCTGGAGCAGCCGGGCTGCGCCCTGGAGCAGCTGGTCCTGTACGACACCTACTG 1301

Qy       3213 CCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCG 3263

Db       1302 GACGGAGGAGGTGGAGGACCGCCTGCAGGCCCTGGAGGGGAGCAAGCCCGG 1352


RESULT 8
US-08-910-731-5
; Sequence 5, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1386 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-910-731-5

  Query Match             4.5%;  Score 182.4;  DB 2;  Length 1386;
  Best Local Similarity   47.1%;  Pred. No. 1.9e-43;
  Matches  595;  Conservative    0;  Mismatches  666;  Indels    3;  Gaps    1;

Qy       2000 GGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCA 2059

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Qy       2060 CCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGA 2119

Db        161 TCAACCCTGCACTGGCAGAGCTCAACCTGCGCAGCAACGAGCTGGGCGATGTCGGCGTGC 220

Qy       2120 AGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAA 2179

Db        221 ATTGCGTGCTCCAGGGCCTGCAGACCCCCTCCTGCAAGATCCAGAAGCTGAGCCTCCAGA 280

Qy       2180 ATGCACAGATTACCC---CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTA 2236

Db        281 ACTGCTGCCTGACGGGGGCCGGCTGCGGGGTCCTGTCCAGCACACTACGCACCCTGCCCA 340

Qy       2237 ACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGT 2296

Db        341 CCCTGCAGGAGCTGCACCTCAGCGACAACCTCTTGGGGGATGCGGGCCTGCAGCTGCTCT 400

Qy       2297 GTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGAT 2356

Db        401 GCGAAGGACTCCTGGACCCCCAGTGCCGCCTGGAAAAGCTGCAGCTGGAGTATTGCAGCC 460

Qy       2357 TGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAAT 2416

Db        461 TCTCGGCTGCCAGCTGCGAGCCCCTGGCCTCCGTGCTCAGGGCCAAGCCGGACTTCAAGG 520

Qy       2417 CTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCT 2476

Db        521 AGCTCACGGTTAGCAACAACGACATCAATGAGGCTGGCGTCCGTGTGCTGTGCCAGGGCC 580

Qy       2477 TGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCA 2536

Db        581 TGAAGGACTCCCCCTGCCAGCTGGAGGCGCTCAAGCTGGAGAGCTGCGGTGTGACATCAG 640

Qy       2537 CGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCC 2596

Db        641 ACAACTGCCGGGACCTGTGCGGCATTGTGGCCTCCAAGGCCTCGCTGCGGGAGCTGGCCC 700

Qy       2597 TATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTC 2656

Db        701 TGGGCAGCAACAAGCTGGGTGATGTGGGCATGGCGGAGCTGTGCCCAGGGCTGCTCCACC 760

Qy       2657 CCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTG 2716

Db        761 CCAGCTCCAGGCTCAGGACCCTGTGGATCTGGGAGTGTGGCATCACTGCCAAGGGCTGCG 820

Qy       2717 GTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGA 2776

Db        821 GGGATCTGTGCCGTGTCCTCAGGGCCAAGGAGAGCCTGAAGGAGCTCAGCCTGGCCGGCA 880

Qy       2777 ACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTC 2836

Db        881 ACGAGCTGGGGGATGAGGGTGCCCGACTGCTGTGTGAGACCCTGCTGGAACCTGGCTGCC 940

Qy       2837 ATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGT 2896

Db        941 AGCTGGAGTCGCTGTGGGTGAAGTCCTGCAGCTTCACAGCCGCCTGCTGCCCCCACTTCA 1000

Qy       2897 CCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGG 2956

Db       1001 GCTCAGTGCTGGCCCAGAACAGGTTTCTCCTGGAGCTACAGATAAGCAACAACAGGCTGG 1060

Qy       2957 GTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGA 3016

Db       1061 AGGATGCGGGCGTGCGGGAGCTGTGCCAGGGCCTGGGCCAGCCTGGCTCTGTGCTGCGGG 1120

Qy       3017 GACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCC 3076

Db       1121 TGCTCTGGTTGGCCGACTGCGATGTGAGTGACAGCAGCTGCAGCAGCCTCGCCGCAACCC 1180

Qy       3077 TTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAG 3136

Db       1181 TGTTGGCCAACCACAGCCTGCGTGAGCTGGACCTCAGCAACAACTGCCTGGGGGACGCCG 1240

Qy       3137 GAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGC 3196

Db       1241 GCATCCTGCAGCTGGTGGAGAGCGTCCGGCAGCCGGGCTGCCTCCTGGAGCAGCTGGTCC 1300

Qy       3197 TGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCA 3256
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Db       1301 TGTACGACATTTACTGGTCTGAGGAGATGGAGGACCGGCTGCAGGCCCTGGAGAAGGACA 1360

Qy       3257 AGCC 3260
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Db       1361 AGCC 1364


RESULT 9
US-08-910-731-7
; Sequence 7, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1371 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
US-08-910-731-7

  Query Match             4.5%;  Score 180.8;  DB 2;  Length 1371;
  Best Local Similarity   47.1%;  Pred. No. 5.5e-43;
  Matches  588;  Conservative    0;  Mismatches  657;  Indels    3;  Gaps    1;

Qy       2016 CCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCG 2075
              |||||  |||||||| ||  | ||  || | ||    ||  |  || ||||   ||||
Db        102 CCTCACGGAGGAGCACTGCAAGGACATCGGTTCTGCCCTCCGGGCCAACCCCTCCCTGAC 161

Qy       2076 GCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAA 2135
                ||||   |||  ||| || |   |||   ||    | | || |      ||
Db        162 CGAGCTCTGCCTCCGCACCAACGAGCTGGGCGATGCCGGCGTGCACCTGGTGCTGCAGGG 221

Qy       2136 GCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCC- 2194
                |||  |  ||||||||||||||| ||||  || |   |    ||         | |||
Db        222 CCTGCAGAGCCCCACCTGCAAGATCCAGAAGCTCAGCCTGCAGAACTGCTCCCTGACCGA 281

Qy       2195 --CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAA 2252
                | ||      | |||   || |  |     ||   |  |  ||  |    || |
Db        282 GGCGGGCTGCGGGGTCCTGCCCAGCACGCTGCGCTCCCTGCCCACGCTGCGGGAGCTGCA 341

Qy       2253 CTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACA 2312
                | | | || ||  |||  ||| |  |   |  || ||   ||||| |   |    |
Db        342 TCTCAGCGACAACCCACTGGGGGACGCCGGCCTGCGGCTGCTCTGTGAGGGGCTCCTGGA 401

Qy       2313 CCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTA 2372
              |||  | ||     |||||    ||  | |||| | |||  |  ||||   ||| | |
Db        402 CCCCCAGTGCCACCTGGAGAAGCTGCAGTTGGAGTACTGCCGCCTGACGGCCGCCAGCTG 461

Qy       2373 CCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGG 2432
                |  |    |  ||    | || | || | |    | ||||   || |   ||
Db        462 CGAGCCCCTGGCCTCGGTGCTCAGGGCCACGCGGGCCTTGAAGGAGCTCACGGTGAGCAA 521

Qy       2433 AAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTG 2492
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Db        522 CAACGACATCGGCGAGGCCGGCGCCCGGGTGCTGGGCCAGGGTCTGGCCGACTCTGCCTG 581

Qy       2493 CGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCT 2552
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Db        582 CCAGCTGGAGACGCTCAGGCTGGAGAACTGCGGTCTCACGCCAGCCAACTGCAAAGACCT 641

Qy       2553 GGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCT 2612
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Db        642 GTGCGGAATTGTGGCCTCCCAGGCCTCGCTGCGGGAGCTGGCCCTGGGCAGCAACAAGCT 701

Qy       2613 GGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCA 2672
              |||  | |  ||  |      |||||  | |    ||   |  |||  ||  || ||
Db        702 GGGTGATGTGGGCATGGCGGAGCTGTGCCCAGGGCTGCTCCACCCCAGCTCCAGGCTCAG 761

Qy       2673 GAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGC 2732
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Db        762 GACCCTGTGGATCTGGGAGTGTGGCATCACTGCCAAGGGCTGCGGGGATCTGTGCCGTGT 821

Qy       2733 GCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAA 2792
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Db        822 CCTCAGGGCCAAGGAGAGCCTGAAGGAGCTCAGCCTGGCCGGCAACGAGCTGGGGGATGA 881

Qy       2793 TGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGA 2852
              || |     || ||||| |||  | ||   |||||    || || ||  ||   |||
Db        882 GGGTGCCCGACTGCTGTGTGAGACCCTGCTGGAACCTGGCTGCCAGCTGGAGTCGCTGTG 941

Qy       2853 GTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAG 2912
              | ||      ||      |||| |||||  |||||           |   ||  |||  |  |
Db        942 GGTGAAGTCCTGCAGCTTCACAGCCGCCTGCTGCCCCCACTTCAGCTCAGTGCTGGCCCA 1001

Qy       2913 GAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGC 2972
              || |||     ||   |   ||  |  | |   ||||     ||||  ||  |  || ||
Db       1002 GAACAGGTTTCTCCTGGAGCTACAGATAAGCAACAACAGGCTGGAGGATGCGGGCGTGCG 1061

Qy       2973 TGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGC 3032
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Db       1062 GGAGCTGTGCCAGGGCCTGGGCCAGCCTGGCTCTGTGCTGCGGGTGCTCTGGTTGGCCGA 1121

Qy       3033 ATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCA 3092
              || |  ||| |     ||||        ||| ||    |||| |    |||||
Db       1122 CTGCGATGTGAGTGACAGCAGCTGCAGCAGCCTCGCCGCAACCCTGTTGGCCAACCACAG 1181

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Db       1182 CCTGCGTGAGCTGGACCTCAGCAACAACTGCCTGGGGGACGCCGGCATCCTGCAGCTGGT 1241

Qy       3153 TTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTA 3212
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Db       1242 GGAGAGCGTCCGGCAGCCGGGCTGCCTCCTGGAGCAGCTGGTCCTGTACGACATTTACTG 1301

Qy       3213 CCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCC 3260
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RESULT 10
US-08-910-731-3
; Sequence 3, Application US/08910731
; Patent No. 5932440
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Mammalian Ribonuclease Inhibitors and Use Thereof
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,731
;      FILING DATE:  (Herewith)
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/795,395
;      FILING DATE:  04-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/794,546
;      FILING DATE:  03-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1374 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-910-731-3

  Query Match             4.4%;  Score 175.8;  DB 2;  Length 1374;
  Best Local Similarity   47.2%;  Pred. No. 1.7e-41;
  Matches  568;  Conservative    0;  Mismatches  632;  Indels    3;  Gaps    1;

Qy       2000 GGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCA 2059
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Qy       2060 CCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGA 2119
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Qy       2120 AGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAA 2179
Db        206 GTCTGGTGCTCCAGGGCCTGCAGAATCCCACTTGTAAGATCCAGAAGCTGAGCCTTCAGA 265

Qy       2180 ATGCACAGATTACCC---CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTA 2236
Db        266 ACTGCAGCTTGACGGAAGCTGGCTGTGGGGTCCTGCCTGATGTGCTGCGCTCTTTGTCTA 325

Qy       2237 ACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGT 2296
Db        326 CCCTGCGTGAACTACATCTCAATGACAACCCTCTGGGGGATGAAGGCCTGAAGCTGCTCT 385

Qy       2297 GTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGAT 2356
Db        386 GTGAAGGACTCCGGGACCCCCAGTGCCGTCTTGAGAAGCTTCAGTTGGAATACTGTAACC 445

Qy       2357 TGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAAT 2416
Db        446 TCACAGCTACCAGCTGCGAGCCCCTGGCCTCAGTGCTCAGGGTGAAACCTGACTTTAAAG 505

Qy       2417 CTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCT 2476
Db        506 AGCTAGTATTGAGCAACAATGACTTCCATGAGGCTGGTATCCACACTCTGTGCCAGGGCC 565

Qy       2477 TGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCA 2536
Db        566 TGAAGGATTCTGCCTGTCAACTGGAGTCACTCAAACTGGAGAACTGTGGTATCACATCAG 625

Qy       2537 CGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCC 2596
Db        626 CCAACTGCAAGGATCTGTGTGATGTTGTGGCCTCCAAAGCCTCACTGCAAGAACTGGACT 685

Qy       2597 TATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTC 2656
Db        686 TGGGCAGCAACAAGCTGGGCAACACAGGCATTGCAGCACTGTGCTCAGGACTGCTGCTTC 745

Qy       2657 CCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTG 2716
Db        746 CCAGCTGCAGGCTGAGGACTCTGTGGCTCTGGGACTGTGATGTCACTGCAGAAGGCTGCA 805

Qy       2717 GTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGA 2776
Db        806 AGGACCTGTGCCGTGTCCTCAGAGCCAAGCAGAGCCTGAAGGAACTCAGCCTAGCTGGCA 865

Qy       2777 ACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTC 2836
Db        866 ATGAGCTGAAGGATGAGGGTGCCCAACTGCTGTGTGAGAGCCTGTTAGAGCCTGGCTGTC 925

Qy       2837 ATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGT 2896
Db        926 AGCTGGAGTCACTGTGGGTAAAGACCTGTAGCCTCACAGCTGCCTCTTGTCCCCACTTCT 985

Qy       2897 CCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGG 2956
Db        986 GCTCGGTGTTGACCAAAAACAGTTCTCTGTTTGAGTTGCAAATGAGCAGCAACCCGCTGG 1045

Qy       2957 GTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGA 3016
Db       1046 GAGACTCGGGAGTCGTGGAGCTTTGCAAGGCCCTGGGCTATCCGGACACAGTGCTGCGTG 1105

Qy       3017 GACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCC 3076
Db       1106 TGCTTTGGCTGGGAGACTGTGATGTGACAGACAGTGGCTGCAGCAGCCTTGCCACTGTCC 1165

Qy       3077 TTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAG 3136
Db       1166 TGCTGGCCAACCGCAGCTTGAGGGAACTGGACCTCAGTAACAACTGCATGGGGGACAACG 1225

Qy       3137 GAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGC 3196
Db       1226 GTGTCCTACAACTGCTGGAGAGCCTCAAACAGCCCAGCTGCATCCTTCAGCAGCTTGTCC 1285

Qy       3197 TGT 3199
Db       1286 TGT 1288


RESULT 11
US-08-795-395-3
; Sequence 3, Application US/08795395
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; Patent No. 5965399
;  GENERAL INFORMATION:
;    APPLICANT:  CHATTERJEE, DEB K.
;    APPLICANT:  SHANDILYA, HARINI
;    TITLE OF INVENTION:  Cloning and Expression of Rat Liver and
;    TITLE OF INVENTION:  Porcine Liver Ribonuclease Inhibitor
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
;      STREET:  1100 NEW YORK AVE., N.W., SUITE 600
;      CITY:  WASHINGTON
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/795,395
;      FILING DATE:  04-FEB-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/024,057
;      FILING DATE:  16-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  0942.3440002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1374 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1368
US-08-795-395-3

  Query Match             4.4%;  Score 175.8;  DB 2;  Length 1374;
  Best Local Similarity   47.2%;  Pred. No. 1.7e-41;
  Matches  568;  Conservative    0;  Mismatches  632;  Indels    3;  Gaps    1;

Qy       2000 GGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCA 2059
             || ||   ||       ||||| ||| | || |||  ||||  || | ||   | |
Db         86 GGCTGGATGACTGTGGCCTCACTGAAGTGCGGTGCAAAGACATCAGGTCAGCGATCCAGG 145

Qy       2060 CCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGA 2119
             || ||||   ||||    ||||   |||  ||| ||     |||   ||    |   ||
Db        146 CCAACCCTGCCCTGACAGAGCTCAGCCTACGCACCAATGAACTGGGTGATGCTGGTGTGG 205

Qy       2120 AGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAA 2179
                ||          |||  | ||||||| || ||||| ||||  ||||   ||   |
Db        206 GTCTGGTGCTCCAGGGCCTGCAGAATCCCACTTGTAAGATCCAGAAGCTGAGCCTTCAGA 265

Qy       2180 ATGCACAGATTACCC---CTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTA 2236
              |       | ||     ||||      |  |||         | |      |      ||
Db        266 ACTGCAGCTTGACGGAAGCTGGCTGTGGGGTCCTGCCTGATGTGCTGCGCTCTTTGTCTA 325

Qy       2237 ACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGT 2296
              |||  |    ||  |  |    | || ||  |||  ||| || |   | | | ||   |
Db        326 CCCTGCGTGAACTACATCTCAATGACAACCCTCTGGGGGATGAAGGCCTGAAGCTGCTCT 385

Qy       2297 GTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGAT 2356
              ||||||   |     ||||  | ||     | |||     |   | |||| | ||||
Db        386 GTGAAGGACTCCGGGACCCCCAGTGCCGTCTTGAGAAGCTTCAGTTGGAATACTGTAACC 445

Qy       2357 TGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAAT 2416
              | ||   | || | | |  |    |  ||  | | || | |       ||   | | |||
Db         446 TCACAGCTACCAGCTGCGAGCCCCTGGCCTCAGTGCTCAGGGTGAAACCTGACTTTAAAG 505

Qy       2417 CTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCT 2476
                ||      ||       ||  |  |     ||    ||  |      |||| |  | | |
Db         506 AGCTAGTATTGAGCAACAATGACTTCCATGAGGCTGGTATCCACACTCTGTGCCAGGGCC 565

Qy       2477 TGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCA 2536
              |||  |  ||    ||   ||| ||  || | |||||| |||||| ||||| |
Db         566 TGAAGGATTCTGCCTGTCAACTGGAGTCACTCAAACTGGAGAACTGTGGTATCACATCAG 625

Qy       2537 CGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCC 2596
              |     ||| ||  ||||      |   | | |  |||         ||  | |  |||  |
Db         626 CCAACTGCAAGGATCTGTGTGATGTTGTGGCCTCCAAAGCCTCACTGCAAGAACTGGACT 685

Qy       2597 TATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTC 2656
              |   || |||||  ||||| ||| |||  |       ||||||    |    ||  |||||
Db         686 TGGGCAGCAACAAGCTGGGCAACACAGGCATTGCAGCACTGTGCTCAGGACTGCTGCTTC 745

Qy       2657 CCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTG 2716
              ||  ||| || |||  ||  |||  |||      | ||  |  |     | |  |||||
Db         746 CCAGCTGCAGGCTGAGGACTCTGTGGCTCTGGGACTGTGATGTCACTGCAGAAGGCTGCA 805

Qy       2717 GTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGA 2776
                ||     | ||  || |  |  ||       | |||| | | || |||||       |
Db         806 AGGACCTGTGCCGTGTCCTCAGAGCCAAGCAGAGCCTGAAGGAACTCAGCCTAGCTGGCA 865

Qy       2777 ACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTC 2836
              |  .  || | ||  | || |   | || |||| |||  | ||  ||| ||    ||||
Db         866 ATGAGCTGAAGGATGAGGGTGCCCAACTGCTGTGTGAGAGCCTGTTAGAGCCTGGCTGTC 925

Qy       2837 ATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGT 2896
              | ||  ||   |||  | |    |  |||   |||| || || |  |||       | |
Db         926 AGCTGGAGTCACTGTGGGTAAAGACCTGTAGCCTCACAGCTGCCTCTTGTCCCCACTTCT 985

Qy       2897 CCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGG 2956
              ||  |||  |  | |  | |||     |||       || |  | |    |||  | ||||
Db         986 GCTCGGTGTTGACCAAAAACAGTTCTCTGTTTGAGTTGCAAATGAGCAGCAACCCGCTGG 1045

Qy       2957 GTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGA 3016
              | |||   || || |  | ||| ||| |||  |||      |   | |||  || |||
Db        1046 GAGACTCGGGAGTCGTGGAGCTTTGCAAGGCCCTGGGCTATCCGGACACAGTGCTGCGTG 1105

Qy       3017 GACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCC 3076
                || || ||  |  ||||  ||||      | ||||      ||  ||   | ||
Db        1106 TGCTTTGGCTGGGAGACTGTGATGTGACAGACAGTGGCTGCAGCAGCCTTGCCACTGTCC 1165

Qy       3077 TTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAG 3136
              |       ||||||     |||      ||  ||||      | ||   | |  |  ||| |
Db        1166 TGCTGGCCAACCGCAGCTTGAGGGAACTGGACCTCAGTAACAACTGCATGGGGGACAACG 1225

Qy       3137 GAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGC 3196
              |  |  |  | |||     |  | |       ||||  |  | | | |||    |||  |
Db        1226 GTGTCCTACAACTGCTGGAGAGCCTCAAACAGCCCAGCTGCATCCTTCAGCAGCTTGTCC 1285

Qy       3197 TGT 3199
              |||
Db        1286 TGT 1288


RESULT 12
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
```

```
;       STREET:  1800 Diagonal Road, Suite 500
;       CITY:  Alexandria
;       STATE:  VA
;       COUNTRY:  USA
;       ZIP:  22313-0299
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/232,463
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/935,313
;       FILING DATE:
;       APPLICATION NUMBER:  EP 91 114 300.6
;       FILING DATE:  26-AUG-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BENT, Stephen A.
;       REGISTRATION NUMBER:  29,768
;       REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703)836-9300
;       TELEFAX:  (703)683-4109
;       TELEX:  899149
;   INFORMATION FOR SEQ ID NO:  14:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  7218 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             1.5%;  Score 61;  DB 1;  Length 7218;
  Best Local Similarity   1.1%;  Pred. No. 1.2e-06;
  Matches    4;  Conservative  225;  Mismatches  130;  Indels    0;  Gaps    0;

Qy        264 GGAGAAGGCACGGGATGACATGAAAAAAATTTCACAAGCTATGGAACAAGAAGGTGCCAC 323
              :::::::: : :::: :: : :::::::::    : :::  : :::: ::::::: :  :
Db       1421 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1362

Qy        324 AGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGC 383
              :: :: ::::: :::::::: ::::::    : :::  : :::: ::::::: :  : ::
Db       1361 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1302

Qy        384 AGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCACGTGAT 443
              :: ::::: ::::::: ::::: : ::::: :: : : :::  : :::::  : : ::
Db       1301 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1242

Qy        444 GACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTG 503
              ::  :::   :  ::::::::::: : : :  : ::    ::::: :  :  :  ::  :
Db       1241 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1182

Qy        504 GCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCG 563
              :  ::::: : ::: :  ::  :: :     ::   :::  :: ::::      ::    :
Db       1181 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1122

Qy        564 CACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCG 622
               : :: ::    : : ::::::  :::::  ::::::  ::    ::  ::::::||||
Db       1121 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCG 1063


RESULT 13
US-09-023-655-395
; Sequence 395, Application US/09023655
; Patent No. 6607879
;  GENERAL INFORMATION:
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Susan G. Stuart
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1508
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,655
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0001 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX: ' (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  395:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  376 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  THP1PLB02
;      CLONE:  153338
US-09-023-655-395

  Query Match             1.5%;  Score 60;  DB 4;  Length 376;
  Best Local Similarity   55.6%;  Pred. No. 3e-07;
  Matches  134;  Conservative    0;  Mismatches  106;  Indels    1;  Gaps    1;

Qy       2914 AGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCT 2973
              | ||||  |  |  |   ||||| || |  ||||| |||||  ||||||    ||  |
Db         35 ACCAGAAGCTGGTTGGAGCTGGACCTGAGTGACAACGCCCTCGGTGACTTCGGAATCAGA 94

Qy       2974 GCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCA 3033
                |||||  | |||||||||||||    |     |   |||||  ||  |||  |||||
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Qy       3034 TGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCAT 3093
              ||  | ||  ||  ||  |  ||  ||| |||  ||  | |  |   |   |  || ||
Db        155 TGCTGCCTCACATCAGCATGTTGTCAGGATCTTNCATCAGTATTGAGCACCAGCCATTCC 214

Qy       3094 CTGACCAG-TCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTG 3152
              ||||||||  ||  |  ||| | |||||  |||  |   |  ||||  |   |  | ||
Db        215 CTGACCAGACCTCTATGTGGGGGAGAATGCCTTGGGAGACTCAGGAGTCGCAATTTTATG 274

Qy       3153 T 3153
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Db        275 T 275


RESULT 14
US-09-949-016-16600
; Sequence 16600, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
```

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;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16600
;   LENGTH: 298336
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(298336)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16600

  Query Match             1.3%;  Score 51.4;  DB 4;  Length 298336;
  Best Local Similarity   58.0%;  Pred. No. 0.011;
  Matches   91;  Conservative    0;  Mismatches   66;  Indels    0;  Gaps    0;

Qy       3273 TGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACACAAAATAGGACTTACTTTCCG 3332
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Db     202167 TTAGAGAATGTGTGATTATTTATTCATTCATGCAGTACACAAGGTAGTTTGGCATTTCCC 202226

Qy       3333 GCTCCCTGAAAGCCGGGCATGGCCATGTGCCTTGCTGTGGGGGATGAACCCAGAGCAGAA 3392
               ||  ||  |      |||| |||||||  |||||| |||   ||||| |  ||  ||||
Db     202227 ATTCTCTATACATTAAGCATAGCCATGTAACTTGCTCTGGTCAATGAATCATGAAAAGAA 202286

Qy       3393 GAAGCGTGTGTCGCTTCTGGCTGGAGACTTCAAGAGC 3429
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Db     202287 GATATATATGTCACATCTGGGAGGAAGCTTTAAGAGC 202323


RESULT 15
US-09-949-016-14581/c
; Sequence 14581, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14581
;   LENGTH: 64309
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(64309)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14581

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  Best Local Similarity   58.7%;  Pred. No. 0.0059;
  Matches   88;  Conservative    0;  Mismatches   62;  Indels    0;  Gaps    0;

Qy        264 GGAGAAGGCACGGGATGACATGAAAAAAATTTCACAAGCTATGGAACAAGAAGGTGCCAC 323
              |||  ||| |  ||| ||   | || ||     | |||     ||| ||||||  |
Db      24025 GGAAGAGGAAGAGGAAGAAGAGGAAGAAGAAGAAAAAGAAGAAGAAGAAGAAGAAGA 23966

Qy        324 AGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGC 383
              || || |||   ||||||| |||||     | |||     ||| ||||||| |    ||
Db      23965 AGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGGAGAAGAAGA 23906

Qy        384 AGCAGAGACAGAAGAACAAGGACATGGAGG 413
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4035	100.0	4035	14	US-10-124-498-5	Sequence 5, Appli
2	4035	100.0	4035	14	US-10-066-521-5	Sequence 5, Appli
3	3166.2	78.5	3885	20	US-10-860-761-3	Sequence 3, Appli
4	3166.2	78.5	3900	17	US-10-399-443-23	Sequence 23, Appl
5	3166.2	78.5	3900	18	US-10-677-943-23	Sequence 23, Appl
6	3139	77.8	3830	15	US-10-216-645-3	Sequence 3, Appli
7	3133.6	77.7	3489	18	US-10-416-642-3	Sequence 3, Appli
8	3133.6	77.7	3926	15	US-10-216-645-1	Sequence 1, Appli
9	2900.6	71.9	3226	18	US-10-092-900A-347	Sequence 347, App
10	1278	31.7	3447	17	US-10-399-443-5	Sequence 5, Appli
11	1278	31.7	3447	18	US-10-677-943-5	Sequence 5, Appli
12	1152.8	28.6	1157	17	US-10-399-443-1	Sequence 1, Appli
13	1152.8	28.6	1157	18	US-10-677-943-1	Sequence 1, Appli
14	756.6	18.8	1075	17	US-10-399-443-3	Sequence 3, Appli
15	756.6	18.8	1075	18	US-10-677-943-3	Sequence 3, Appli
16	729.4	18.1	3521	20	US-10-794-342-2	Sequence 2, Appli
17	438	10.9	2775	17	US-10-357-820-51	Sequence 51, Appl
18	424	10.5	2985	10	US-09-965-621-15	Sequence 15, Appl
19	424	10.5	2985	17	US-10-407-866-15	Sequence 15, Appl
20	424	10.5	2985	19	US-10-781-294-15	Sequence 15, Appl
21	422.4	10.5	2982	14	US-10-124-498-25	Sequence 25, Appl
22	422.4	10.5	2982	14	US-10-066-521-25	Sequence 25, Appl
23	422.4	10.5	3190	17	US-10-094-749-1079	Sequence 1079, Ap
24	422.4	10.5	3368	14	US-10-124-498-23	Sequence 23, Appl
25	422.4	10.5	3368	14	US-10-066-521-23	Sequence 23, Appl
26	419.2	10.4	2575	9	US-09-848-035-7	Sequence 7, Appli
27	419.2	10.4	2575	9	US-09-986-224-7	Sequence 7, Appli
28	419.2	10.4	2883	17	US-10-161-493-3	Sequence 3, Appli
29	419.2	10.4	3172	19	US-10-398-037-74	Sequence 74, Appl
30	409	10.1	3186	14	US-10-124-498-17	Sequence 17, Appl
31	409	10.1	3186	14	US-10-066-521-17	Sequence 17, Appl
32	404.4	10.0	3108	10	US-09-965-621-23	Sequence 23, Appl
33	404.4	10.0	3108	17	US-10-407-866-23	Sequence 23, Appl
34	404.4	10.0	3108	19	US-10-781-294-23	Sequence 23, Appl
35	404.4	10.0	3218	17	US-10-407-866-67	Sequence 67, Appl
36	392.6	9.7	3189	15	US-10-239-663-10	Sequence 10, Appl
37	392.6	9.7	4944	22	US-10-499-353A-429	Sequence 429, App
38	390.6	9.7	3540	20	US-10-794-342-7	Sequence 7, Appli
39	381.4	9.5	3099	13	US-10-127-516-3	Sequence 3, Appli
40	381.4	9.5	3099	13	US-10-027-629-3	Sequence 3, Appli
41	381.4	9.5	3099	16	US-10-132-967-3	Sequence 3, Appli
42	381.4	9.5	3431	13	US-10-127-516-1	Sequence 1, Appli
43	381.4	9.5	3431	13	US-10-027-629-1	Sequence 1, Appli
44	381.4	9.5	3431	16	US-10-132-967-1	Sequence 1, Appli
45	368.4	9.1	2763	19	US-10-250-615-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-10-124-498-5
; Sequence 5, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; CURRENT FILING DATE:' 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4035
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(4032)
US-10-124-498-5

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Query Match             100.0%;  Score 4035;  DB 14;  Length 4035;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 4035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
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Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
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Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300

Qy        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360

Qy        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420
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Db        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420

Qy        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480
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Db        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480

Qy        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540
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Db        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540

Qy        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600
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Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

Qy        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720
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Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780
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Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140

Qy       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200
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Db       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200

Qy       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260

Qy       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320

Qy       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380

Qy       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440

Qy       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500

Qy       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560

Qy       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620

Qy       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680

Qy       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTG 1740

Qy       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800
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Db       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800

Qy       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860

Qy       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920

Qy       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
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Db       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980

Qy       1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040

Qy       2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100

Qy       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
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Db       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Qy       2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
Db       2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
Qy       2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
Db       2221 GTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAG 2280
Qy       2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
Db       2281 GATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGG 2340
Qy       2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
Db       2341 CTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACC 2400
Qy       2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
Db       2401 TCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATG 2460
Qy       2461 CCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGAC 2520
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Qy       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
Db       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
Qy       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Db       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
Qy       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Db       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Qy       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Db       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
Qy       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
Db       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
Qy       2821 AGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCG 2880
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Qy       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
Db       2881 TGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTC 2940
Qy       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
Db       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
Qy       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Db       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
Qy       3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
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Qy       3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
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Qy       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
Db       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
Qy       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
Db       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
Qy       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
Db       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
Qy       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
Db       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
Qy       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Db       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Qy       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
Db       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
Qy       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
Db       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
Qy       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
Db       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
Qy       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
Db       3661 GAGCTGAGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGT 3720
Qy       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
Db       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
Qy       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
Db       3781 GTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGTGCTGATGAC 3840
Qy       3841 CACAGCGGTGTGGCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTGTCCAACAGT 3900
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Qy       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
Qy       3961 TCCAACAGTGCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAG 4020
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Qy       4021 GGGCTGGTGTCTTAA 4035
Db       4021 GGGCTGGTGTCTTAA 4035
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RESULT 2
US-10-066-521-5
; Sequence 5, Application US/10066521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-334001
; CURRENT APPLICATION NUMBER: US/10/066,521
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10

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;  PRIOR APPLICATION NUMBER: 60/265,231
;  PRIOR FILING DATE: 2001-01-31
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 4035
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(4032)
US-10-066-521-5

  Query Match             100.0%;  Score 4035;  DB 14;  Length 4035;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 4035;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
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Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
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Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
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Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
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Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300

Qy        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360
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Db        301 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCT 360

Qy        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420
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Db        361 ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACA 420

Qy        421 TGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGT 480
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Qy        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540
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Db        481 TTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCA 540

Qy        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600
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Db        541 GACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAA 600

Qy        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660
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Db        601 TCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATG 660

Qy        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720
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Db        661 TTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTC 720

Qy        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCC 780

Qy        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAAC 840

Qy        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900
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Db        841 AATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGC 900

Qy        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTG 960

Qy        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATC 1020

Qy       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACA 1080

Qy       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCC 1140

Qy       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCC 1200

Qy       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260
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Db       1201 CCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCT 1260

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Db       1261 CGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGC 1320

Qy       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATG 1380

Qy       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCA 1440

Qy       1441 GACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCC 1500
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Qy       1501 GCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTT 1560
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Qy       1561 GAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680
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Db       1621 ATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTG 1680

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Qy       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800
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Db       1741 GGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTC 1800

Qy       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860
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Db       1801 GAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTT 1860

Qy       1861 CCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTAT 1920
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Qy       1921 TTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCA 1980
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Qy       1981 TGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGAT 2040
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Qy       2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Db       2041 TTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATC 2100
Qy       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Db       2101 CTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATA 2160
Qy       2161 CAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATC 2220
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Qy       2521 TGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGC 2580
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Qy       2581 TTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGT 2640
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Qy       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Db       2641 CGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTG 2700
Qy       2701 GACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCAC 2760
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Qy       2761 CTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATG 2820
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Qy       2941 ACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAG 3000
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Qy       3001 AACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAG 3060
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Qy       3061 GCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAAT 3120
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Qy       3121 AACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAAC 3180
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Qy       3181 TTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAG 3240
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Qy       3241 GAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAA 3300
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Qy       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
Db       3301 GATGACCGACACAAAATAGGACTTACTTTCCGGCTCCCTGAAAGCCGGGCATGGCCATGT 3360
Qy       3361 GCCTTGCTGTGGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
Db       3361 GCCTTGCTGTGGGGGATGAACCCAGAGCAGAAGAAGCGTGTGTCGCTTCTGGCTGGAGAC 3420
Qy       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Db       3421 TTCAAGAGCAGTACACGATTTGCCAAGTCTCTCTGCCTGGCCACGGCAAATGGTGAGTCC 3480
Qy       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
Db       3481 CAGAGAGTTGACAACGTGGAGCAGAGCTCCCCGCAACCCATGGCAGGCACGGAACACAAA 3540
Qy       3541 CAAGATAAAATGTTGAGTGTTGGATATTCCGGAGCCTGGTCTGAAACTGCTGAGCTCGAA 3600
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Qy       3601 GGGCTTGGATCCAACAGTGCTGATCATGACCACGGAGGTATGGCCTGGTCACTAGGGAGA 3660
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Qy       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
Db       3721 CACTGGGAGCGGCTGGGCTCTAGGGGCTGGTGTCTTAACAGTGCTGATGACCACAGCGGT 3780
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Db       3901 GCTGATGACCACAGCGGTGTGTCCTGGTCACTGGGAGCGGCTGGGCTCGAGGGGCTTGTG 3960
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Db       4021 GGGCTGGTGTCTTAA 4035
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RESULT 3
US-10-860-761-3

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; Sequence 3, Application US/10860761
; Publication No. US20040248775A1
; GENERAL INFORMATION:
;  APPLICANT: WYETH
;  TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS
;  FILE REFERENCE: AM101318
;  CURRENT APPLICATION NUMBER: US/10/860,761
;  CURRENT FILING DATE:  2004-06-03
;  NUMBER OF SEQ ID NOS: 31
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 3885
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(3603)
US-10-860-761-3

  Query Match             78.5%;  Score 3166.2;  DB 20;  Length 3885;
  Best Local Similarity   96.2%;  Pred. No. 0;
  Matches 3304;  Conservative    0;  Mismatches    8;  Indels  123;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
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Db        154 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 213

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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Db        274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453

Qy        290 ---------------------------------------------------------- 289

Db        454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513

Qy        290 ----------------------------------------------------AAATTTCA 297
                                                                   ||||||||
Db        514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573

Qy        298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633

Qy        358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
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Db        634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693

Qy        418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
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Qy        478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
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Qy        598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
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Db        874 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 933

Qy        658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
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Qy        718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
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Qy        778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
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Qy        838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
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Qy        898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
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Qy        958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
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Qy       1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
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Db       1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353

Qy       1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
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Qy       1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
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Qy       1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
              ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db       1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533

Qy       1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
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Db       1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593

Qy       1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
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Qy       1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
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Qy       1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
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Db       1714 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1773

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Qy       1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
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Qy       1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
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Db       1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953

Qy       1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
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Qy       1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
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Qy       1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
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Qy       1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193

Qy       1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2194 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 2253

Qy       1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
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Db       2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313

Qy       2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373

Qy       2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
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Db       2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433

Qy       2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
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Db       2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493

Qy       2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
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Db       2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553

Qy       2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
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Db       2554 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2613

Qy       2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
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Db       2614 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2673

Qy       2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457
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Qy       2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517
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Db       2734 ACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2793

Qy       2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
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Db       2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
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Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
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Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
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Db       2974 CTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 3033

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
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Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
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Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
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Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
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Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
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Db       3334 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3393

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Db       3394 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3453

Qy       3178 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3237
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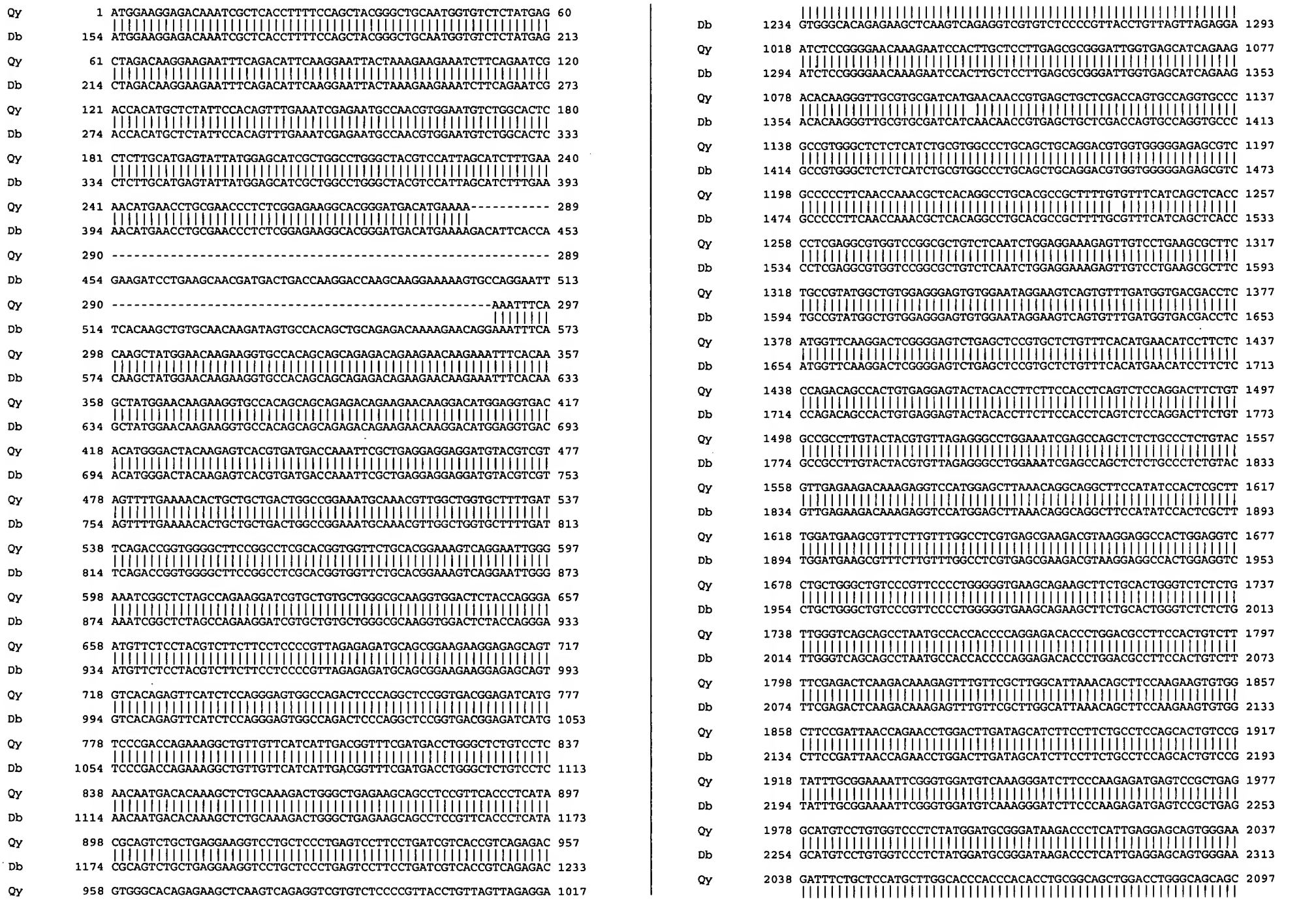
RESULT 4
US-10-399-443-23
; Sequence 23, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
; OTHER INFORMATION:
US-10-399-443-23

Query Match 78.5%; Score 3166.2; DB 17; Length 3900;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3304; Conservative 0; Mismatches 8; Indels 123; Gaps 1;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Qy 61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
Db 214 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 273
Qy 121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
Db 274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333
Qy 181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
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Qy 241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
Db 394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453
Qy 290 ---------- 289
Db 454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513
Qy 290 ----------AAATTTCA 297
Db 514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573
Qy 298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
Db 574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633
Qy 358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
Db 634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693
Qy 418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
Db 694 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 753
Qy 478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
Db 754 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 813
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Qy 598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
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Qy 658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
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Qy 958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
Db 1234 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1293
Qy 1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
Db 1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353
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Qy 1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
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Qy 1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
Db 1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593
Qy 1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
Db 1594 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1653
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Qy 1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
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Qy 1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
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Qy 1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
Db 1834 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1893
Qy 1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
Db 1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953
Qy 1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
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Db 2074 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 2133
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Db 2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193
Qy 1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
Db 2194 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 2253
Qy 1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
Db 2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313
Qy 2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097

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Db       2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373

Qy       2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
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Db       2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433

Qy       2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
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Db       2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493

Qy       2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553

Qy       2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
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Db       2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
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Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
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Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
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Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
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Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 3213

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
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Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
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Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

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Db       3574 GAAGATGACCGGTAC 3588
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RESULT 5
US-10-677-943-23
; Sequence 23, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 3900
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3600)
US-10-677-943-23

Query Match 78.5%; Score 3166.2; DB 18; Length 3900;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 3304; Conservative 0; Mismatches 8; Indels 123; Gaps 1;

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Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 213

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 273

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 333

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 393

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAGACATTCACCA 453

Qy        290 ---------- 289

Db        454 GAAGATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGGAATT 513
```

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Qy       290 ----------------------------------------------------AAATTTCA 297
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Db       514 TCACAAGCTGTGCAACAAGATAGTGCCACAGCTGCAGAGACAAAAGAACAGGAAATTTCA 573

Qy       298 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 357
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       574 CAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAA 633

Qy       358 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 417
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       634 GCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGAC 693

Qy       418 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 477
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       694 ACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGT 753

Qy       478 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 537
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       754 AGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGAT 813

Qy       538 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 597
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       814 TCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGG 873

Qy       598 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 657
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       874 AAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGA 933

Qy       658 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 717
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       934 ATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGT 993

Qy       718 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 777
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       994 GTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATG 1053

Qy       778 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 837
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1054 TCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC 1113

Qy       838 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 897
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1114 AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATA 1173

Qy       898 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1174 CGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGAC 1233

Qy       958 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1017
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1234 GTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGA 1293

Qy      1018 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1294 ATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAG 1353

Qy      1078 ACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1137
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      1354 ACACAAGGGTTGCGTGCGATCATCAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCC 1413

Qy      1138 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1414 GCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTC 1473

Qy      1198 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACC 1257
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db      1474 GCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGCGTTTCATCAGCTCACC 1533

Qy      1258 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1534 CCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTC 1593

Qy      1318 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1594 TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTC 1653

Qy      1378 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1654 ATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTC 1713

Qy      1438 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1714 CCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGT 1773

Qy      1498 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1774 GCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTAC 1833

Qy      1558 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1617
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1834 GTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTT 1893

Qy      1618 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1677
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1894 TGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTC 1953

Qy      1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1954 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 2013

Qy      1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2014 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 2073

Qy      1798 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 1857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2074 TTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGG 2133

Qy      1858 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 1917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2134 CTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCG 2193

Qy      1918 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 1977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2194 TATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAG 2253

Qy      1978 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2254 GCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAA 2313

Qy      2038 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2314 GATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGC 2373

Qy      2098 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2374 ATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAG 2433

Qy      2158 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGA 2217
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db      2434 ATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAACACCTCTGGAGA 2493

Qy      2218 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2277
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Db      2494 ATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAA 2553

Qy      2278 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2337
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2554 GAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTG 2613

Qy      2338 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2614 AGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACG 2673

Qy      2398 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       2674 ACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTA 2733

Qy       2458 ATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2517
              | |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db       2734 ACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAG 2793

Qy       2518 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2794 GACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGG 2853

Qy       2578 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2854 AGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTG 2913

Qy       2638 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2914 TGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCAC 2973

Qy       2698 CTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 2757
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       2974 CTGGACACGGCTGGCTGTGGTTCTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACG 3033

Qy       2758 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 2817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3034 CACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTC 3093

Qy       2818 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 2877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3094 ATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCC 3153

Qy       2878 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 2937
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3154 GCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGAT 3213

Qy       2938 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 2997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3214 CTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAA 3273

Qy       2998 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3274 AAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGT 3333

Qy       3058 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3117
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||-
Db       3334 GAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAG 3393

Qy       3118 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3394 AATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCT 3453

Qy       3178 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3237
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3454 AACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTG 3513

Qy       3238 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3297
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Db       3514 GAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGAT 3573

Qy       3298 GAAGATGACCGACAC 3312
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Db       3574 GAAGATGACCGGTAC 3588


RESULT 6
US-10-216-645-3
; Sequence 3, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
;  APPLICANT: WEISS, BERTRAM
;  APPLICANT:  LESSL, MONIKA
;  APPLICANT:  PETERS-KOTTIG, MICHAELE
;  APPLICANT:  BECKMANN, GEORG
;  TITLE OF INVENTION: HUMAN MATER PROTEINS
;  FILE REFERENCE: SCH-1910
;  CURRENT APPLICATION NUMBER: US/10/216,645
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3830
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-216-645-3

  Query Match             77.8%;  Score 3139;  DB 15;  Length 3830;
  Best Local Similarity   96.0%;  Pred. No. 0;
  Matches 3282;  Conservative    0;  Mismatches   30;  Indels  105;  Gaps    2;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
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Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
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Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAAAATTTCACAA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||     || ||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300

Qy        301 GCT---------------ATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACA- 344
              | ||               |  || |||| |     ||  | |  || | ||||| |  |
Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

Qy        345 ------------------------------------------------------------ 344

Db        361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420

Qy        345 ----------------------------AGAAATTTCACAAGCTATGGAACAAGAAGGT 375
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Qy        376 GCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGT 435
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Db        481 GCCACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGT 540

Qy        436 CACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CACGTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCT 600

Qy        496 GCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCTGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTC 660

Qy        556 CGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGA 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGGCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGA 720

Qy        616 AGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTC 675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGGATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTC 780

Qy        676 TTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCC 735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCC 840
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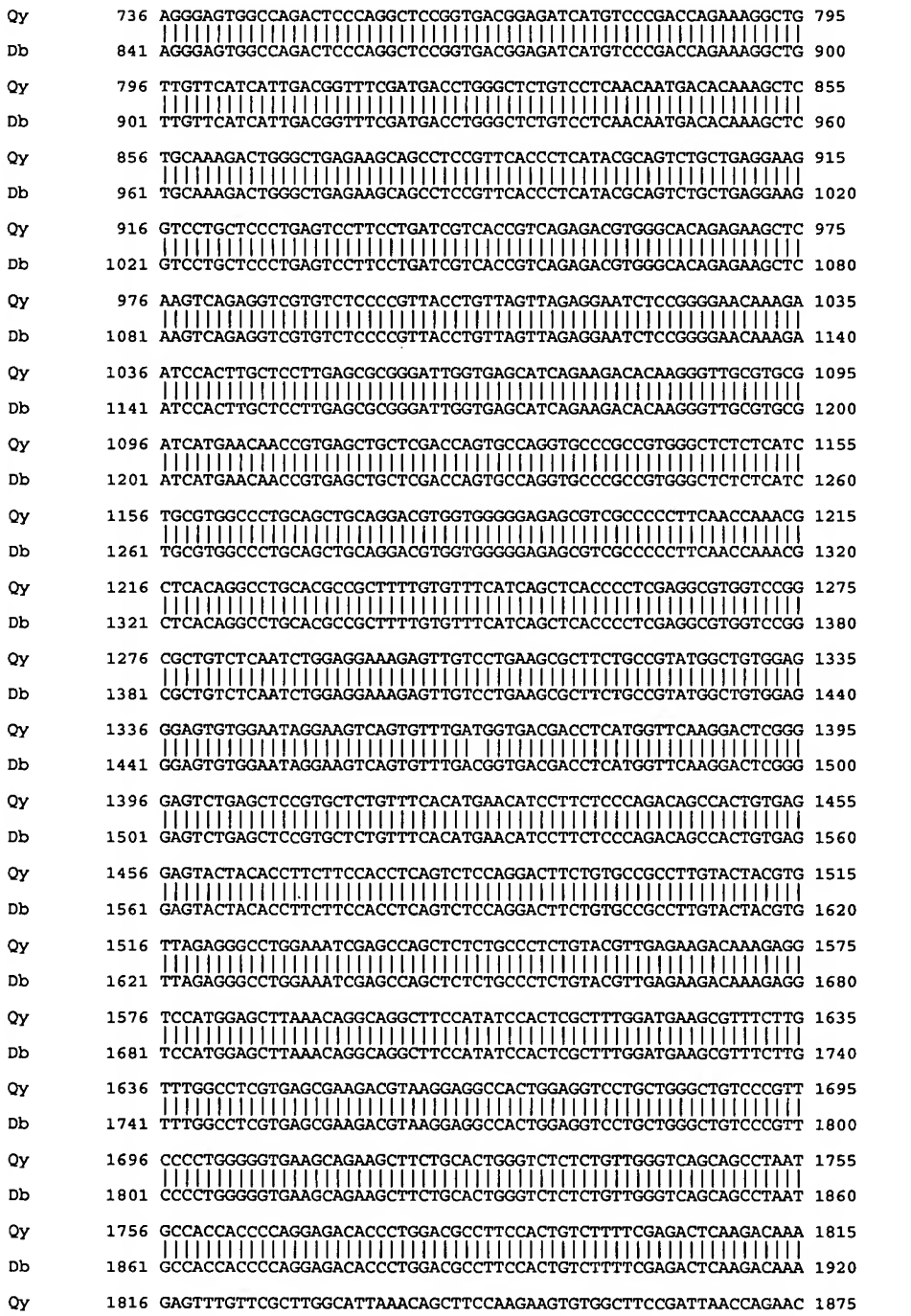
Qy 736 AGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTG 795
Db 841 AGGGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTG 900
Qy 796 TTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTC 855
Db 901 TTGTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTC 960
Qy 856 TGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAG 915
Db 961 TGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAG 1020
Qy 916 GTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTC 975
Db 1021 GTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTC 1080
Qy 976 AAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGA 1035
Db 1081 AAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGA 1140
Qy 1036 ATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCG 1095
Db 1141 ATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCG 1200
Qy 1096 ATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATC 1155
Db 1201 ATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATC 1260
Qy 1156 TGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACG 1215
Db 1261 TGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACG 1320
Qy 1216 CTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGG 1275
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Qy 1276 CGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAG 1335
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Qy 1336 GGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGG 1395
Db 1441 GGAGTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGG 1500
Qy 1396 GAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAG 1455
Db 1501 GAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAG 1560
Qy 1456 GAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTG 1515
Db 1561 GAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTG 1620
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Qy 1576 TCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTG 1635
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Qy 1756 GCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAA 1815
Db 1861 GCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAA 1920
Qy 1816 GAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAAC 1875
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Qy 1876 CTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGG 1935
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Qy 1936 GTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCT 1995
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Qy 1996 CTATGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTT 2055
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Qy 2236 AACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCG 2295
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Qy 2476 TTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCC 2535
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Db 2821 GGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATG 2880
Qy 2776 AACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGT 2835
Db 2881 AACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGT 2940
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Db 2941 CATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTG 3000
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Qy       2956 GGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACG 3015
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Db       3061 GGTGACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACG 3120

Qy       3016 AGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCC 3075
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Db       3121 AGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCC 3180

Qy       3076 CTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAA 3135
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Db       3181 CTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAA 3240

Qy       3136 GGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGG 3195
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Qy       3196 CTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTC 3255
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Qy       3256 AAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
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RESULT 7
US-10-416-642-3
; Sequence 3, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  ARVIZU, Chandra
;  TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
;  FILE REFERENCE: PF-0842 PCT
;  CURRENT APPLICATION NUMBER: US/10/416,642
;  CURRENT FILING DATE:  2003-05-13
;  PRIOR APPLICATION NUMBER: 60/249,407
;  PRIOR FILING DATE: 2000-11-15
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PERL Program
; SEQ ID NO 3
;   LENGTH: 3489
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CB1
US-10-416-642-3

  Query Match             77.7%;  Score 3133.6;  DB 18;  Length 3489;
  Best Local Similarity   95.2%;  Pred. No. 0;
  Matches 3308;  Conservative    0;  Mismatches    4;  Indels  162;  Gaps    1;

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Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
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Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
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Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300

Qy        290 ---------------------------------------------------------- 289

Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

Qy        290 ---------------------------------------------------------- 289

Db        361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420

Qy        290 ----------------------------AAATTTCACAAGCTATGGAACAAGAAGGT 318
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Db        421 AAGTATGTTGGAATTCATTCTTCTTTTGCAGAAATTTCACAAGCTATGGAACAAGAAGGT 480

Qy        319 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 540

Qy        379 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 600

Qy        439 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 498
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Db        601 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 660

Qy        499 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 558
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Db        661 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 720

Qy        559 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 618
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Db        721 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 780

Qy        619 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 678
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Db        781 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 840

Qy        679 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 738
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 900

Qy        739 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 960

Qy        799 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 858
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Db        961 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 1020

Qy        859 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 918
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Db       1021 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 1080

Qy        919 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 978
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Db       1081 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 1140

Qy        979 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATC 1038
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Db       1141 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATC 1200

Qy       1039 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1098
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Db       1201 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1260

Qy       1099 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1158
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Db       1261 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1320

Qy       1159 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1218
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Db       1321 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1380
Qy       1219 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1278
Db       1381 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1440
Qy       1279 TGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGA 1338
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Qy       1339 GTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1398
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Qy       1399 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1458
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Qy       1519 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1578
Db       1681 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1740
Qy       1579 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1638
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Qy       1699 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1758
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Db       1981 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 2040
Qy       1879 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 1938
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Qy       1999 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2058
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Qy       2419 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2478
Db       2581 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2640
Qy       2479 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2538
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Qy       2539 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2598
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Qy       2719 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2778
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Qy       3199 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3258
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RESULT 8
US-10-216-645-1
; Sequence 1, Application US/10216645

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; Publication No. US20030125282A1
; GENERAL INFORMATION:
;  APPLICANT: WEISS, BERTRAM
;  APPLICANT:  LESSL, MONIKA
;  APPLICANT:  PETERS-KOTTIG, MICHAELE
;  APPLICANT:  BECKMANN, GEORG
;  TITLE OF INVENTION: HUMAN MATER PROTEINS
;  FILE REFERENCE: SCH-1910
;  CURRENT APPLICATION NUMBER: US/10/216,645
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 3926
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-216-645-1

  Query Match             77.7%;  Score 3133.6;  DB 15;  Length 3926;
  Best Local Similarity   95.2%;  Pred. No. 0;
  Matches 3308;  Conservative    0;  Mismatches    4;  Indels  162;  Gaps    1;

Qy          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAAGGAGACAAATCGCTCACCTTTTCCAGCTACGGGCTGCAATGGTGTCTCTATGAG 60

Qy         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTAGACAAGGAAGAATTTCAGACATTCAAGGAATTACTAAAGAAGAAATCTTCAGAATCG 120

Qy        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACCACATGCTCTATTCCACAGTTTGAAATCGAGAATGCCAACGTGGAATGTCTGGCACTC 180

Qy        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTCTTGCATGAGTATTATGGAGCATCGCTGGCCTGGGCTACGTCCATTAGCATCTTTGAA 240

Qy        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAA---------- 289
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AACATGAACCTGCGAACCCTCTCGGAGAAGGCACGGGATGACATGAAAAATTCACCAGAA 300

Qy        290 ---------------------------------------------------------- 289

Db        301 GATCCTGAAGCAACGATGACTGACCAAGGACCAAGCAAGGAAAAAGTGCCAGAAAATAAA 360

Qy        290 ---------------------------------------------------------- 289

Db        361 TATGGCATGACTAAGCTTATCTTGGGGGTGTCTGACATCTCTGACTCGAATAATAAACAC 420

Qy        290 ------------------------------AAATTTCACAAGCTATGGAACAAGAAGGT 318
                                           |||||||||||||||||||||||||||||
Db        421 AAGTATGTTGGAATTCATTCTTCTTTTGCAGAAATTTCACAAGCTATGGAACAAGAAGGT 480

Qy        319 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 378
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCACAGCAGCAGAGACAGAAGAACAAGAAATTTCACAAGCTATGGAACAAGAAGGTGCC 540

Qy        379 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 438
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Db        541 ACAGCAGCAGAGACAGAAGAACAAGGACATGGAGGTGACACATGGGACTACAAGAGTCAC 600

Qy        439 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGATGACCAAATTCGCTGAGGAGGAGGATGTACGTCGTAGTTTTGAAAACACTGCTGCT 660

Qy        499 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 558
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCGG 720

Qy        559 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 618
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGG 780

Qy        619 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 678
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTC 840

Qy        679 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 738
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Db        841 CTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGG 900

Qy        739 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 798
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTG 960

Qy        799 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 858
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGC 1020

Qy        859 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 918
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTC 1080

Qy        919 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 978
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAG 1140

Qy        979 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATC 1038
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Db       1141 TCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATC 1200

Qy       1039 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1098
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Db       1201 CACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATC 1260

Qy       1099 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1158
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Db       1261 ATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGC 1320

Qy       1159 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1218
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Db       1321 GTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTC 1380

Qy       1219 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1278
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Db       1381 ACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGC 1440

Qy       1279 TGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGA 1338
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Qy       1339 GTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1398
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Db       1501 GTGTGGAATAGGAAGTCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAG 1560

Qy       1399 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1458
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Db       1561 TCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAG 1620

Qy       1459 TACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTA 1518
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Db       1621 TACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTA 1680

Qy       1519 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1578
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Db       1681 GAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCC 1740

Qy       1579 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1638
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Db       1741 ATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTT 1800

Qy       1639 GGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCC 1698
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Db       1801 GGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCC 1860

Qy       1699 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1758
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCC 1920

Qy       1759 ACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAG 1818
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Db       1921 ACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAG 1980

Qy       1819 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 1878
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Db       1981 TTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTG 2040

Qy       1879 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 1938
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Db       2041 GACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTG 2100

Qy       1939 GATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTA 1998
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Db       2101 GATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTA 2160

Qy       1999 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 TGGATGCGGGATAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGC 2220

Qy       2059 ACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATG 2118
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Db       2221 ACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATG 2280

Qy       2119 AAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGA 2178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 AAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGA 2340

Qy       2179 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2238
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Db       2341 AATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAAC 2400

Qy       2239 CTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGT 2298
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Qy       2299 GAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTG 2358
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Qy       2359 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2418
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Db       2521 ACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCT 2580

Qy       2419 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2478
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Db       2581 CTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTG 2640

Qy       2479 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 AGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACG 2700

Qy       2539 GGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTA 2598
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Qy       2599 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2658
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Db       2761 TCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCC 2820

Qy       2659 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2718
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Db       2821 CACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGT 2880

Qy       2719 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2778
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Db       2881 TTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAAC 2940

Qy       2779 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 2838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 CCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCAT 3000

Qy       2839 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 2898
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Db       3001 CTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCC 3060

Qy       2899 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 2958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGT 3120

Qy       2959 GACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3018
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db       3121 GACGGTGGGGTTGCTGCACTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGA 3180

Qy       3019 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 CTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTT 3240

Qy       3079 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 TCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGA 3300

Qy       3139 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3198
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Db       3301 ATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTG 3360

Qy       3199 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3258
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Db       3361 TGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAG 3420

Qy       3259 CCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
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RESULT 9
US-10-092-900A-347
; Sequence 347, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernev,, Velizar T.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.

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;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-290C
;  CURRENT APPLICATION NUMBER: US/10/092,900A
;  CURRENT FILING DATE:  2002-03-07
;  PRIOR APPLICATION NUMBER: USSN 60/274,322
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/283,675
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: USSN 60/338,092
;  PRIOR FILING DATE: 2001-12-03
;  PRIOR APPLICATION NUMBER: USSN 60/274,281
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/274,191
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/325,681
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: USSN 60/304,354
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: USSN 60/279,995
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: USSN 60/294,899
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: USSN 60/287,424
;  PRIOR FILING DATE: 2001-04-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 347
;   LENGTH: 3226
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (69)..(3168)
US-10-092-900A-347

  Query Match            71.9%;  Score 2900.6;  DB 18;  Length 3226;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches 2903;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        406 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 465
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Db        249 CATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAG 308

Qy        466 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCT 368

Qy        526 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 585
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Db        369 GGTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAG 428

Qy        586 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 488

Qy        646 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 705
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Db        489 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 548

Qy        706 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 765
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 AAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGTG 608

Qy        766 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 ACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCTG 668

Qy        826 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 885
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Db        669 GGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCG 728

Qy        886 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTC 788

Qy        946 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 1005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 ACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTG 848

Qy       1006 TTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 1065
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 TTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGT 908

Qy       1066 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 1125
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Db        909 GAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAG 968

Qy       1126 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 TGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTG 1028

Qy       1186 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1245
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Db       1029 GGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTT 1088

Qy       1246 CATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTC 1305
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Qy       1306 CTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGAT 1365
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Qy       1366 GGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATG 1425
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Qy       1426 AACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTC 1485
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Qy       1546 TGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCAT 1605
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Db       1449 ATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGG 1508

Qy       1666 CCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCAC 1725
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Qy       1726 TGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCC 1785
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Db       1569 TGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCC 1628

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Db       1629 TTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTC 1688

Qy       1846 CAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTTCTGCCTC 1905
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Qy       1906 CAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCCAAGAGAT 1965
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Qy       1966 GAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAG 2025
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Db       1809 GAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATGGATGCGGGATAAGACCCTCATTGAG 1868

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Qy       2146 CCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAG 2205
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Db       2049 CACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACC 2108

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Qy       2326 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2385
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Db       2169 TTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCC 2228

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Db       2529 AATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAAC 2588

Qy       2746 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2805
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Db       2589 TCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTT 2648

Qy       2806 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2865
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Db       2649 CTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGT 2708

Qy       2866 CATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTG 2925
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Qy       2926 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAG 2985
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Db       2769 AAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCACTGTGCGAG 2828

Qy       2986 GGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACT 3045
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Db       2829 GGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACT 2888

Qy       3046 TCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTA 3105
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RESULT 10
US-10-399-443-5
; Sequence 5, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 3447
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-399-443-5

Query Match 31.7%; Score 1278; DB 17; Length 3447;
Best Local Similarity 67.2%; Pred. No. 0;
Matches 1898; Conservative 0; Mismatches 908; Indels 18; Gaps 6;

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Qy        678 CCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAG 737
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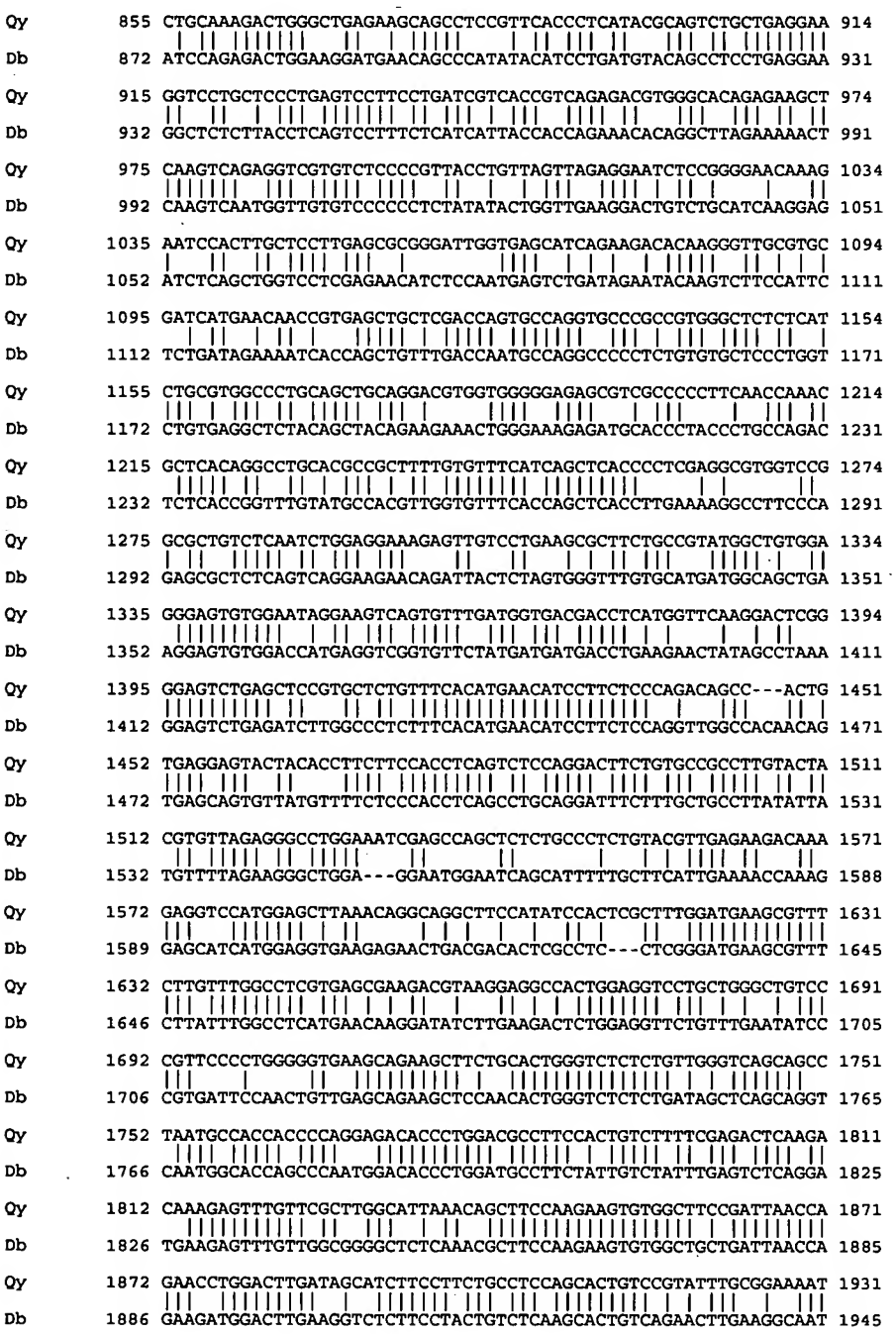
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Qy 2769 TAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACC 2828
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Db       3026 CCTGAGGAGACTTGGGTTGGGGGCATGTAAGTTGACTTCCAATTGCTGTGAGGCATTGTC 3085

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Db       3266 GTTTGTCAAGCCCCACGTGGTGATTGATGGTGATTGGTATGCTAGTGATGAAGATGACCG 3325

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RESULT 11
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; Sequence 5, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 3447
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-677-943-5

  Query Match             31.7%;  Score 1278;  DB 18;  Length 3447;
  Best Local Similarity   67.2%;  Pred. No. 0;
  Matches 1898;  Conservative    0;  Mismatches  908;  Indels   18;  Gaps    6;

Qy        498 TGACTGGCCGGAAATGCAAACGTTGGCTGGTGCTTTTGATTCAGACCGGTGGGGCTTCCG 557

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Qy        558 GCCTCGCACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAG 617

Db        575 GCCTCACACCATTATCCTACATGGAAGACCAGGAGTTGGGAAGTCAGCTTTGGCCAGAAG 634

Qy        618 GATCGTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTT 677

Db        635 TATTGTTCTTGGCTGGGCACAGGGTAAACTCTTCCAAAAAATG---TCCTTTGTCATCTT 691

Qy        678 CCTCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAG 737

Db        692 CTTCTCTGTTAGAGAAATAAAGTGGACAGAGAAGAGCAGTTTGGCACAGCTGATTGCTAA 751

Qy        738 GGAGTGGCCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTT 797

Db        752 GGAGTGTCCAGACTCCTGGGATCTAGTGACAAAGATCATGTCCCAACCAGAAAGACTCTT 811

Qy        798 GTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCCTC---AACAATGACACAAAGCT 854

Db        812 GTTTGTCATAGATGGCTTGGATGATATGGACTCTGTCCTCCAACATGATGATATGACACT 871

Qy        855 CTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAA 914

Db        872 ATCCAGAGACTGGAAGGATGAACAGCCCATATACATCCTGATGTACAGCCTCCTGAGGAA 931

Qy        915 GGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCT 974

Db        932 GGCTCTCTTACCTCAGTCCTTTCTCATCATTACCACCAGAAACACAGGCTTAGAAAAACT 991

Qy        975 CAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAG 1034

Db        992 CAAGTCAATGGTTGTGTCCCCCCTCTATATACTGGTTGAAGGACTGTCTGCATCAAGGAG 1051

Qy       1035 AATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGC 1094

Db       1052 ATCTCAGCTGGTCCTCGAGAACATCTCCAATGAGTCTGATAGAATACAAGTCTTCCATTC 1111

Qy       1095 GATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCAT 1154

Db       1112 TCTGATAGAAAATCACCAGCTGTTTGACCAATGCCAGGCCCCCTCTGTGTGCTCCCTGGT 1171

Qy       1155 CTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAAC 1214

Db       1172 CTGTGAGGCTCTACAGCTACAGAAGAAACTGGGAAAGAGATGCACCCTACCCTGCCAGAC 1231

Qy       1215 GCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCG 1274

Db       1232 TCTCACCGGTTTGTATGCCACGTTGGTGTTTCACCAGCTCACCTTGAAAAGGCCTTCCCA 1291

Qy       1275 GCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGA 1334

Db       1292 GAGCGCTCTCAGTCAGGAAGAACAGATTACTCTAGTGGGTTTGTGCATGATGGCAGCTGA 1351

Qy       1335 GGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGG 1394

Db       1352 AGGAGTGTGGACCATGAGGTCGGTGTTCTATGATGATGACCTGAAGAACTATAGCCTAAA 1411

Qy       1395 GGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAGACAGCC---ACTG 1451

Db       1412 GGAGTCTGAGATCTTGGCCCTCTTTCACATGAACATCCTTCTCCAGGTTGGCCACAACAG 1471

Qy       1452 TGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTA 1511

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Qy       1512 CGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAA 1571

Db       1532 TGTTTTAGAAGGGCTGGA---GGAATGGAATCAGCATTTTTGCTTCATTGAAAACCAAAG 1588

Qy       1572 GAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTT 1631

Db       1589 GAGCATCATGGAGGTGAAGAGAACTGACGACACTCGCCTC---CTCGGGATGAAGCGTTT 1645

Qy       1632 CTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCC 1691

Db       1646 CTTATTTGGCCTCATGAACAAGGATATCTTGAAGACTCTGGAGGTTCTGTTTGAATATCC 1705

Qy       1692 CGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCC 1751

Db       1706 CGTGATTCCAACTGTTGAGCAGAAGCTCCAACACTGGGTCTCTCTGATAGCTCAGCAGGT 1765

Qy       1752 TAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGA 1811

Db       1766 CAATGGCACCAGCCCAATGGACACCCTGGATGCCTTCTATTGTCTATTTGAGTCTCAGGA 1825

Qy       1812 CAAAGAGTTTGTTCGCTTGGCATTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCA 1871
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Db       1826 TGAAGAGTTTGTTGGCGGGGCTCTCAAACGCTTCCAAGAAGTGTGGCTGCTGATTAACCA 1885

Qy       1872 GAACCTGGACTTGATAGCATCTTCCTTCTGCCTCCAGCACTGTCCGTATTTGCGGAAAAT 1931

Db       1886 GAAGATGGACTTGAAGGTCTCTTCCTACTGTCTCAAGCACTGTCAGAACTTGAAGGCAAT 1945

Qy       1932 TCGGGTGGATGTCAAAGGGATCTTCCCAAGAGATGAGTCCGCTGAGGCATGTCCTGTGGT 1991

Db       1946 CCGGGTGGATATCAGAGACCTCCTCTCGGTAGATAATACTCTCGAGCTGTGCCCTGTTGT 2005

Qy       1992 CCCTCTATGGATGCGGGA---TAAGACCCTCATTGAGGAGCAGTGGGAAGATTTCTGCTC 2048

Db       2006 TACTGTCCAGGAGACACAATGTAAGCCCCTCCTCATGGAGTGGTGGGGAAACTTCTGCTC 2065

Qy       2049 CATGCTTGGCACCCACCCACACCTGCGGCAGCTGGACCTGGGCAGCAGCATCCTGACAGA 2108

Db       2066 TGTGCTTGGCAGCCTCCGGAACTTGAAGGAGCTGGACTTGGGCGACAGCATCCTGAGTCA 2125

Qy       2109 GCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATACAGACCCT 2168

Db       2126 ACGGGCCATGAAGATACTGTGCCTCGAGCTGCGGAATCAGTCCTGCAGAATACAGAAGCT 2185

Qy       2169 GATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGC 2228

Db       2186 GACGTTTAAGAGTGCAGAGGTAGTGTCTGGCCTGAAACATCTCTGGAAGCTCCTTTTTAG 2245

Qy       2229 CAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAG 2288

Db       2246 CAATCAAAACTTAAAGTACCTCAATCTAGGGAACACTCCCATGAAGGATGATGACATGAA 2305

Qy       2289 GATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGCTGGATTG 2348

Db       2306 GTTAGCCTGCGAAGCGCTGAAACATCCAAAGTGCTCCGTGGAGACTCTGAGGTTGGATTC 2365

Qy       2349 CTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCCAG 2408

Db       2366 CTGTGAGTTAACCATCATTGGTTATGAGATGATCTCCACGCTTCTTATTTCAACCACCAG 2425

Qy       2409 CCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGCCTCTCAG 2468

Db       2426 GCTAAAGTGTCTCAGCCTGGCCAAAAATAGAGTGGGAGTAAAAAGCATGATATCCCTTGG 2485

Qy       2469 TGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCAT 2528

Db       2486 GAATGCCTTGAGTAGCTCAATGTGTCTACTGCAAAAGTTGATACTGGACAACTGTGGCCT 2545

Qy       2529 CACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACA 2588

Db       2546 CACACCTGCCAGCTGCCACCTTCTGGTCTCAGCCCTTTTCAGCAACCAGAACTTGACACA 2605

Qy       2589 CCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCAT 2648

Db       2606 CCTGTGCCTGTCAAACAACAGCCTGGGGACTGAAGGAGTGCAACAGCTGTGTCAGTTCCT 2665

Qy       2649 GAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGC 2708

Db       2666 GAGGAATCCAGAATGTGCTCTCCAGCGGCTGATACTGAATCACTGCAACATTGTAGATGA 2725

Qy       2709 TGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCT 2768

Db       2726 TGCTTATGGCTTCCTGGCAATGAGACTTGCAAACAACACAAAGCTGACCCACCTGAGCCT 2785

Qy       2769 TAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACC 2828

Db       2786 GACCATGAACCCCGTAGGGGATGGTGCAATGAAGCTACTGTGTGAAGCTTTAAAGGAACC 2845

Qy       2829 ATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGA 2888

Db       2846 TACTTGTTACCTTCAAGAACTGGAACTAGTGGACTGCCAACTCACACAGAACTGCTGCGA 2905

Qy       2889 GAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAA 2948

Db       2906 GGACCTGGCCTGTATGATCACAACAACCAAGCACTTAAAAAGTTTGGATCTTGGTAACAA 2965

Qy       2949 TGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGT 3008

Db       2966 CGCCCTGGGTGACAAAGGAGTCATAACCCTGTGTGAGGGACTGAAGCAAAGTAGCAGCTC 3025

Qy       3009 TCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTC 3068

Db       3026 CCTGAGGAGACTTGGGTTGGGGGCATGTAAGTTGACTTCCAATTGCTGTGAGGCATTGTC 3085

Qy       3069 CTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAG 3128

Db       3086 ATTGGCCATCTCTTGCAACCCTCACCTGAACAGCCTAAACCTGGTGAAGAATGACTTCAG 3145

Qy       3129 TCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGAT 3188

Db       3146 TACATCGGGGATGTTGAAGCTGTGCTCTGCGTTCCAATGCCCTGTCTCTAACCTGGGGAT 3205

Qy       3189 AATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCA 3248

Db       3206 AATTGGCCTGTGGAAGCAGGAGTACTATGCCCGAGTGAGAAGACAGCTGGAGGAAGTTGA 3265

Qy       3249 GCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCG 3308

Db       3266 GTTTGTCAAGCCCCACGTGGTGATTGATGGTGATTGGTATGCTAGTGATGAAGATGACCG 3325

Qy       3309 ACAC 3312

Db       3326 AAAC 3329
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RESULT 12
US-10-399-443-1
; Sequence 1, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-443-1

Query Match 28.6%; Score 1152.8; DB 17; Length 1157;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1154; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy        814 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 873

Db         61 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 120

Qy        874 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 933

Db        121 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 180
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Qy        934 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 240

Qy        994 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 300

Qy       1054 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 360

Qy       1114 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 420

Qy       1174 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 1233
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Db        421 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 480

Qy       1234 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 1293
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 540

Qy       1294 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 600

Qy       1354 TCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 1413
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Db        601 TCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 660

Qy       1414 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 1473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 720

Qy       1474 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 1533
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Db        721 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 780

Qy       1534 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 1593
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Db        781 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 840

Qy       1594 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 1653
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Db        841 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 900

Qy       1654 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 1713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 960

Qy       1714 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1773
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Db        961 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1020

Qy       1774 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1833
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Db       1021 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1080

Qy       1834 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1893
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Db       1081 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1140

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RESULT 13
US-10-677-943-1
; Sequence 1, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 1157
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-677-943-1

  Query Match             28.6%;  Score 1152.8;  DB 18;  Length 1157;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1154;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        754 CAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 813
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Db          1 CAAGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGT 60

Qy        814 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 873
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Db         61 TTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGACTGGGCTGAG 120

Qy        874 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCC 180

Qy        934 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 993
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Db        181 TTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCT 240

Qy        994 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 1053
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Db        241 CCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAG 300

Qy       1054 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAG 360

Qy       1114 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 1173
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Db        361 CTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTG 420

Qy       1174 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 1233
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Db        421 CAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCC 480

Qy       1234 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 1293
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Db        481 GCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAG 540

Qy       1294 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 1353
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Db        541 GAAAGAGTTGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAG 600

Qy       1354 TCAGTGTTTGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 1413
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Db        601 TCAGTGTTTGACGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCT 660
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Qy       1414 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 1473
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Db        661 CTGTTTCACATGAACATCCTTCTCCCAGACAGCCACTGTGAGGAGTACTACACCTTCTTC 720

Qy       1474 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 1533
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Db        721 CACCTCAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATC 780

Qy       1534 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 1593
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Db        781 GAGCCAGCTCTCTGCCCTCTGTACGTTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAG 840

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Db        841 GCAGGCTTCCATATCCACTCGCTTTGGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAA 900

Qy       1654 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 1713
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACGTAAGGAGGCCACTGGAGGTCCTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAG 960

Qy       1714 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1773
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Db        961 AAGCTTCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGAC 1020

Qy       1774 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1833
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCCTGGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCA 1080

Qy       1834 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1893
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Db       1081 TTAAACAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCT 1140

Qy       1894 TCCTTCTGCCTCCAGC 1909
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Db       1141 TCCTTCTGCCTCCAGC 1156
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RESULT 14
US-10-399-443-3
; Sequence 3, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as Represented by the
; APPLICANT: Secretary, Department of Health & Human Services, The National Institute
; APPLICANT: Health
; APPLICANT: Nelson, Lawrence M.
; APPLICANT: Tong, Zhi-Bin
; APPLICANT: Nelson, Lawrence
; APPLICANT: Zhi-Bin, Tong
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64785
; CURRENT APPLICATION NUMBER: US/10/399,443
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1075
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-399-443-3

Query Match 18.8%; Score 756.6; DB 17; Length 1075;
Best Local Similarity 99.5%; Pred. No. 6e-218;
Matches 759; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       2550 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 2609
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Qy       2610 CGTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 2669
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Qy       2790 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 2849
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2850 GGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 2909
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Qy       3030 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 3089
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Db        481 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 540

Qy       3090 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 3149
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Db        541 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 600

Qy       3150 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 3209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 660

Qy       3210 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 3269
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Qy       3270 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
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RESULT 15
US-10-677-943-3
; Sequence 3, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1075

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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-677-943-3

  Query Match             18.8%;  Score 756.6;  DB 18;  Length 1075;
  Best Local Similarity   99.5%;  Pred. No. 6e-218;
  Matches  759;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2550 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 2609
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAG 60

Qy       2610 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 2669
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Db         61 CCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCT 120

Qy       2670 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACT 2729
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        121 GCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTCTCTTGCACT 180

Qy       2730 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 2789
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGA 240

Qy       2790 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 2849
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Db        241 CAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCT 300

Qy       2850 GGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 2909
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGAGTTGGTAAAATGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTC 360

Qy       2910 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 2969
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Db        361 GAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGT 420

Qy       2970 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 3029
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAA 480

Qy       3030 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 3089
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Db        481 GGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCG 540

Qy       3090 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 3149
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Db        541 GCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCT 600

Qy       3150 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 3209
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCA 660

Qy       3210 GTACCCTGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGT 3269
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Qy       3270 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
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Db        721 AATTGACGGTAGTTGGCATTCTTTTGATGAAGATGACCGGTAC 763


Search completed: July 19, 2005, 02:27:12
Job time : 2360 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 18, 2005, 16:09:10 ; Search time 12236 Seconds
(without alignments)
12552.250 Million cell updates/sec

Title: US-10-066-521-5
Perfect score: 4035
Sequence: 1 atggaaggagacaaatcgct.....tcgaggggctggtgtcttaa 4035

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1261	31.3	3475	3	AK087774	AK087774 Mus muscu
	2	723.8	17.9	791	7	CK000513	CK000513 AGENCOURT
	3	422.4	10.5	3359	3	BC021272	BC021272 Homo sapi
	4	422.4	10.5	3360	3	BC012789	BC012789 Homo sapi
	5	402.8	10.0	814	6	CB228956	CB228956 AGENCOURT
	6	381.4	9.5	776	7	CO814088	CO814088 AGENCOURT
	7	377.8	9.4	1913	3	AK016782	AK016782 Mus muscu
	8	374.4	9.3	808	7	CO804754	CO804754 AGENCOURT
c	9	358.2	8.9	693	5	BU634350	BU634350 UI-H-FL1-
c	10	357.2	8.9	684	5	BU630481	BU630481 UI-H-FL0-
	11	349.2	8.7	786	7	CO802335	CO802335 AGENCOURT
	12	336	8.3	792	7	CO382844	CO382844 AGENCOURT
	13	323.4	8.0	1119	4	BM454123	BM454123 AGENCOURT
	14	320	7.9	739	7	CO815646	CO815646 AGENCOURT
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	16	284.8	7.1	701	7	CO801395	CO801395 AGENCOURT
	17	282.4	7.0	817	7	CO797627	CO797627 AGENCOURT
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	19	276.6	6.9	3577	3	AK087843	AK087843 Mus muscu
	20	267.2	6.6	3218	3	AK054378	AK054378 Mus muscu
	21	256.2	6.3	666	1	AV367637	AV367637 AV367637
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c	23	242	6.0	565	4	BM226108	BM226108 K0222C06-
	24	238.2	5.9	589	6	CA559886	CA559886 K0264H01-
	25	232.6	5.8	552	7	CN724433	CN724433 E0879B11-
	26	232.2	5.8	583	6	CA559979	CA559979 K0266B01-
	27	231.2	5.7	593	6	CA558845	CA558845 K0250F09-
c	28	230.6	5.7	768	7	CO808001	CO808001 AGENCOURT
	29	229.8	5.7	643	7	CF913803	CF913803 B0954D05-
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c	31	221.4	5.5	515	4	BM227562	BM227562 K0245E10-
	32	221.4	5.5	4123	3	HSM800983	AL117470 Homo sapi
c	33	221	5.5	511	4	BM230035	BM230035 K0288H05-
c	34	221	5.5	512	4	BM226240	BM226240 K0225A02-
c	35	219.8	5.4	513	4	BM227869	BM227869 K0250F09-
c	36	218.6	5.4	519	4	BG071729	BG071729 H3102E07-
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	38	217.8	5.4	559	6	CA561556	CA561556 K0288H05-
	39	216.2	5.4	743	7	CK635847	CK635847 UI-M-HN0-
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ALIGNMENTS

RESULT 1
AK087774
LOCUS AK087774 3475 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330019F16 product:mouse MATER protein (maternal-antigen-that-embryos-require). protein, full insert sequence.
ACCESSION AK087774
VERSION AK087774.1 GI:26104500
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5

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  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3475)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
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            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/
            URL:http://fantom.gsc.riken.jp/.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:10090"
                     /clone="E330019F16"
                     /sex="female"
                     /tissue_type="ovary"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
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                     (maternal-antigen-that-embryos-require) protein
                     putative"
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ORIGIN

  Query Match             31.3%;  Score 1261;  DB 3;  Length 3475;
  Best Local Similarity   65.3%;  Pred. No. 0;
  Matches 1982;  Conservative    0;  Mismatches 1035;  Indels   20;  Gaps    8;

Qy        287 AAAAAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAG 346
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Qy        347 AAATTTCACAAGCTATGGAACAAGAAGGTGCCACAGCAGCAGAGACAGAAGAACAAGGAC 406
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Db        384 AAAGAAAAATGACTTCTCCAGAAAACGACAGTAAATCAATCCAGAAAGACCAAGGACCAG 443

Qy        407 ATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACCAAATTCGCTGAGGAGGAGG 466
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Qy        467 ATGTACGTCGTAGTTTTGAAAACACTGCTGCTGACTGGCCGGAAATGCAAACGTTGGCTG 526
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Qy        527 GTGCTTTTGATTCAGACCGGTGGGGCTTCCGGCCTCGCACGGTGGTTCTGCACGGAAAGT 586
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Qy        587 CAGGAATTGGGAA-ATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAAGGTGGA 645
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Qy        646 CTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCCGTTAGAGAGATGCAGCGGAAG 705
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Db        684 CTCTTCCAAAAAATG---TCCTTTGTCATCTTCTTCTCTGTTAGAGAAATAAAGTGGACA 740

Qy        706 AAGGAGAGCAGTGTCACAGAG-TTCATCTCCAGGGAGTGGCCAGACTCCCAGGCTCCGGT 764
              ||  ||||||||  |  || ||  | ||  | | |||||| ||||||||||  || ||  ||
Db        741 GAGAAGAGCAGTTTGGCACAGCCTGATTGCTAAGGAGTGTCCAGACTCCTGGGATCTAGT 800

Qy        765 GACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGATGACCT 824
              |||  |||||||||||| |||||||| || | |||  |||| || || || |||||  |
Db        801 GACAAAGATCATGTCCCAACCAGAAAGACTCTGGTTTGTCATAGATGGCTTGGATGATAT 860

Qy        825 GGGCTCTGTCCTC---AACAATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCC 881
              ||  ||||||||||    |  |||| |  |  || | || |||||||   ||  | |||||
Db        861 GGACTCTGTCCTCCAACATGATGATATGACACTATCCAGAGACTGGAAGGATGAACAGCC 920

Qy        882 TCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGAT 941
                | || ||| ||   ||| || |||||||||  || || ||| ||||||| || ||
Db        921 CATATACATCCTGATGTACAGCCTCCTGAGGAAGGCTCTCCTACCTCAGTCCTTTCTCAT 980

Qy        942 CGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTA 1001
              | | |||  |||| ||   |||  ||| || |||||||||  ||| |||| |||| ||
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Qy       1002 CCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGAT 1061
                | | |||  |||| | || |    |  |||   ||  || |||| |||  |
Db       1041 TATACTGGTTGAAGGACTGTCTGCATCAAGGAGATCTCAGCTGGTCCTCGAGAACATCTC 1100

Qy       1062 TGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGA 1121
              ||||  | | |  | ||||| || | | |  | ||  | ||  |  |||| | ||
Db       1101 CAATGAGTCTGATAGAATACAAGTCTTCCATTCTCTGATAGAAAATCACCAGCTGTTTGA 1160

Qy       1122 CCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGT 1181
              ||| |||||||  ||| | ||| |||| ||  |||| | ||| || ||||| ||| |
Db       1161 CCAATGCCAGGCCCCCTCTGTGTGCTCCCTGGTCTGTGAGGCTCTACAGCTACAGAAGAA 1220

Qy       1182 GGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGT 1241
                |||| ||||   | |||    |  ||| || ||||| ||  || | ||| | || ||
Db       1221 ACTGGGAAAGAGATGCACCCTACCCTGCCAGACTCTCACCGGTTTGTATGCCACGTTGGT 1280

Qy       1242 GTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGT 1301
              ||||||  |||||||||      | |       || | ||  ||||| || ||| |||    |
Db       1281 GTTTCACCAGCTCACCTTGAAAAGGCCTTCCCAGAGCGCTCTCAGTCAGGAAGAACAGAT 1340

Qy       1302 TGTCCTGAAGCGCTTCTGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTT 1361
              |   ||   | | || |||   ||||| |  || ||||||||||  | || ||| |||||
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Qy       1362 TGATGGTGACGACCTCATGGTTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCA 1421
                ||| ||| ||||| | |    |  | ||   |||||||||| ||   || || |||||
Db       1401 CTATGATGATGACCTGAAGAACTATAGCCTAAAGGAGTCTGAGATCTTGGCCCTCTTTCA 1460

Qy       1422 CATGAACATCCTTCTCCCAGACAGCC---ACTGTGAGGAGTACTACACCTTCTTCCACCT 1478
              ||||||||||||||||||  |  |||   || ||||| |||   ||    |||| ||||||
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Qy       1479 CAGTCTCCAGGACTTCTGTGCCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCC 1538
              ||| || ||||| |||| ||| ||||| || || || ||||| || |||||    ||
Db       1521 CAGCCTGCAGGATTTCTTTGCTGCCTTATATTATGTTTTAGAAGGGCTGGA---GGAATG 1577

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Db       1638 CGACACTCGCCTC---CTCGGGATGAAGCGTTTCTTATTTGGCCTCATGAACAAGGATAT 1694

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Db       1695 CTTGAAGACTCTGGAGGTTCTGTTTGAATATCCCGTGATTCCAACTGTTGAGCAGAAGCT 1754

Qy       1719 TCTGCACTGGGTCTCTCTGTTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCT 1778

Db       1755 CCAACACTGGGTCTCTCTGATAGCTCAGCAGGTCAATGGCACCAGCCCAATGGACACCCT 1814

Qy       1779 GGACGCCTTCCACTGTCTTTTCGAGACTCAAGACAAAGAGTTTGTTCGCTTGGCATTAAA 1838

Db       1815 GGATGCCTTCTATTGTCTATTTGAGTCTCAGGATGAAGAGTTTGTTGGCGGGGCTCTCAA 1874

Qy       1839 CAGCTTCCAAGAAGTGTGGCTTCCGATTAACCAGAACCTGGACTTGATAGCATCTTCCTT 1898

Db       1875 ACGCTTCCAAGAAGTGTGGCTGCTGATTAACCAGAAGATGGACTTGAAGGTCTCTTCCTA 1934

Qy       1899 CTGCCTCCAGCACTGTCCGTATTTGCGGAAAATTCGGGTGGATGTCAAAGGGATCTTCCC 1958

Db       1935 CTGTCTCAAGCACTGTCAGAACTTGAAGGCAATCCGGGTGGATATCAGAGACCTCCTCTC 1994

Qy       1959 AAGAGATGAGTCCGCTGAGGCATGTCCTGTGGTCCCTCTATG---GATGCGGGATAAGAC 2015

Db       1995 GGTAGATAATACTCTCGAGCTGTGCCCTGTTGTTACTGTCCGGGAGACACAATGTAAGCC 2054

Qy       2016 CCTCATTGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCCACCCACACCTGCG 2075

Db       2055 CCTCCTCATGGAGTGGTGGGGAAACTTCTGCTCTGTGCTTGGCAGCCTCCGGAACTTGAA 2114

Qy       2076 GCAGCTGGACCTGGGCAGCAGCATCCTGACAGAGCGGGCCATGAAGACCCTGTGTGCCAA 2135

Db       2115 GGAGCTGGACTTGGGCGACAGCATCCTGAGTCAACGGGCCATGAAGATACTGTGCCTCGA 2174

Qy       2136 GCTGAGGCATCCCACCTGCAAGATACAGACCCTGATGTTTAGAAATGCACAGATTACCCC 2195

Db       2175 GCTGCGGAATCAGTCCTGCAGAATACAGAAGCTGACGTTTAAGAGTGCAGAGGTAGTGTC 2234

Qy       2196 TGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGATCCCTCAACTT 2255

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Qy       2256 GGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGCCTTAAAACACCC 2315

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Qy       2316 AAAATGTTTGTTGGAGTCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCT 2375

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Qy       2376 GAAGATCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAA 2435

Db       2415 GATGATCTCCACGCTTCTTATTTCAACCACCAGGCTAAAGTGTCTCAGCCTGGCCAAAAA 2474

Qy       2436 CAAGGTGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGC 2495

Db       2475 TAGAGTGGGAGTAAAAAGCATGATATCCCTTGGGAATGCCTTGAGTAGCTCAATGTGTCT 2534

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Db       2535 ACTGCAAAAGTTGATACTGGACAACTGTGGCCTCACACCTGCCAGCTGCCACCTTCTGGT 2594

Qy       2556 CTCAGCCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGG 2615

Db       2595 CTCAGCCCTTTTCAGCAACCAGAACTTGACACACCTGTGCCTGTCAAACAACAGCCTGGG 2654

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Qy       2676 GCTGATGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCT 2735

Db       2715 GCTGATACTGAATCACTGCAACATTGTAGATGATGCTTATGGCTTCCTGGCAATGAGACT 2774

Qy       2736 TATGGGTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGG 2795

Db       2775 TGCAAACAACACAAAGCTGACCCACCTGAGCCTGACCATGAACCCCGTAGGGGATGGTGC 2834

Qy       2796 CGTGAAGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTT 2855

Db       2835 AATGAAGCTACTGTGTGAAGCTTTAAAGGAACCTACTTGTTACCTTCAAGAACTGGAACT 2894

Qy       2856 GGTAAAGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAG 2915

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Qy       2916 CAGACACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGC 2975

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Qy       3036 TGGACTGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCT 3095

Db       3075 TAAGTTGACTTCCAATTGCTGTGAGGCATTGTCATTGGCCATCTCTTGCAACCCTCACCT 3134

Qy       3096 GACCAGTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTC 3155

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Qy       3156 GGCCTTTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCC 3215

Db       3195 TGCGTTCCAATGCCCTGTCTCTAACCTGGGGATAATTGGCCTGTGGAAGCAGGAGTACTA 3254

Qy       3216 TGTGCAAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGA 3275

Db       3255 TGCCCGAGTGAGAAGACAGCTGGAGGAAGTTGAGTTTGTCAAGCCCCACGTGGTGATTGA 3314

Qy       3276 CGGTAGTTGGCATTCTTTTGATGAAGATGACCGACAC 3312

Db       3315 TGGTGATTGGTATGCTAGTGATGAAGATGACCGAAAC 3351
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RESULT 2
CK000513

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LOCUS       CK000513                 791 bp    mRNA    linear   EST 26-NOV-2003
DEFINITION  AGENCOURT_16368905 NIH_MGC_221 Homo sapiens cDNA clone
            IMAGE:30708637 5', mRNA sequence.
ACCESSION   CK000513
VERSION     CK000513.1  GI:38526547
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 791)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin, University of Iowa
             cDNA Library Preparation: M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
```

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           http://image.llnl.gov
           Plate: NDAM1075  row: c  column: 14
           High quality sequence stop: 688.
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                     /clone="IMAGE:30708637"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_221"
                     /note="Organ: mixed; Vector: pYX-Asc; Site_1: EcoRI;
                     Site_2: NotI; Library is oligo-dT primed and directionally
                     cloned Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according tomRNA size fraction, ligated with
                     EcoR I adaptor, digested with Not I and then cloned
                     directionally into pYX-Asc vector. Average insert size
                     4-5Kb. Adaptors 5'(AATTCGGCACGAGG)3' and 5'd
                     (CCTCGTGCCG)3'. 3' Linker sequence - GCGGCCGCTGAGAGCC T18.
                     Sequencing primers 3'end: T3 promoter primer 5'd
                     (ATTAACCCTCACTAAAGGGA)3'. 5' End: T7 promoter primer 5'd
                     (TAATACGACTCACTATAGGG)3'. Library was constructed in the
                     laboratory of M. Bento Soares. Note: this is a NIH_MGC
                     Library"
ORIGIN

  Query Match             17.9%;  Score 723.8;  DB 7;  Length 791;
  Best Local Similarity   99.1%;  Pred. No. 1.6e-188;
  Matches  780;  Conservative    0;  Mismatches    2;  Indels    5;  Gaps    5;

Qy        565 ACGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTG 624
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 AGGGTGGTTCTGCACGGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTG 64

Qy        625 CTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCC 684
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 CTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCCTACGTCTTCTTCCTCCCC 124

Qy        685 GTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGG 744
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 GTTAGAGAGATGCAGCGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGG 184

Qy        745 CCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATC 804
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Db        185 CCAGACTCCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATC 244

Qy        805 ATTGACGGTTTCGATGACCTGGGCTCTGTCCTCAACAATGACACAAAGCTCTGCAAAGAC 864
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Qy        865 TGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTC 924
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Qy        925 CCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAG 984
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Db        365 CCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAG 424

Qy        985 GTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTG 1044
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Db        425 GTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGGAACAAAGAATCCACTTG 484

Qy       1045 CTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAAC 1104
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Db        485 CTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACACAAGGGTTGCGTGCGATCATGAAC 544

Qy       1105 AACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCGTGGGCTCTCTCATCTGCGTGGCC 1164
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Qy       1165 CTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCCCCTTCAACCAAACGCTCACAGGC 1224
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Qy       1225 CTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTC 1284
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Db        665 CTGCACGCCGCTTTTGTGTTT-ATCAGCTCACCCCTCGAGGCGTGGTCCGGCGCTGTCTC 723

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Db        724 AATCTGGAGG-AAGAGTTGTCCTG-AGCGCTTCTGCCGT-TGGCTGTGGA-GGAGTGTGG 779

Qy       1345 AATAGGA 1351
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Db        780 AATAAGA 786


RESULT 3
BC021272
LOCUS       BC021272               3359 bp    mRNA    linear   HTC 12-OCT-2004
DEFINITION  Homo sapiens cDNA clone IMAGE:4811303, containing frame-shift
            errors.
ACCESSION   BC021272
VERSION     BC021272.2  GI:33878145
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3359)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
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            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 3359)
  AUTHORS   Director MGC Project.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JAN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Aug 19, 2003 this sequence version replaced gi:18204229.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 39 Row: g Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19745161
This clone has the following problem: frame shifted.

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ORIGIN

Query Match 10.5%; Score 422.4; DB 3; Length 3359;
Best Local Similarity 50.2%; Pred. No. 9.5e-105;
Matches 1261; Conservative 0; Mismatches 1206; Indels 45; Gaps 7;

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Qy       580 GGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATCGTGCTGTGCTGGGCGCAA 639
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Qy       700 CGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCT 759
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Qy       760 CCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGAT 819
Db       704 CCTATAACAGAGATCGTGTCTCAACCGGAGAGACTCTTGTTCGTCATCGACAGCTTCGAA 763

Qy       820 GACCTGGGCTCTGTCCTCAACAAT---GACACAAAGCTCTGCAAAGACTGGGCTGAGAAG 876
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Qy       877 CAGCCTCCGTTCACCCTCATACGCAGTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTC 936
Db       824 CGGCCGGTGCAGGTGCTTCTGAGCAGTTTGCTGAGGAAGAAGATGCTCCCGGAGGCCTCC 883

Qy       937 CTGATCGTCACCGTCAGAGACGTGGGCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCC 996
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ACCESSION   BC012789
VERSION     BC012789.2  GI:33872518
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3360)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
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  AUTHORS   Director MGC Project.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     On Aug 19, 2003 this sequence version replaced gi:15215377.
            Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 25 Row: k Column: 23
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 19745161
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ORIGIN
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Qy        700 CGGAAGAAGGAGAGCAGTGTCACAGAGTTCATCTCCAGGGAGTGGCCAGACTCCCAGGCT 759

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Qy        760 CCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTGTTGTTCATCATTGACGGTTTCGAT 819
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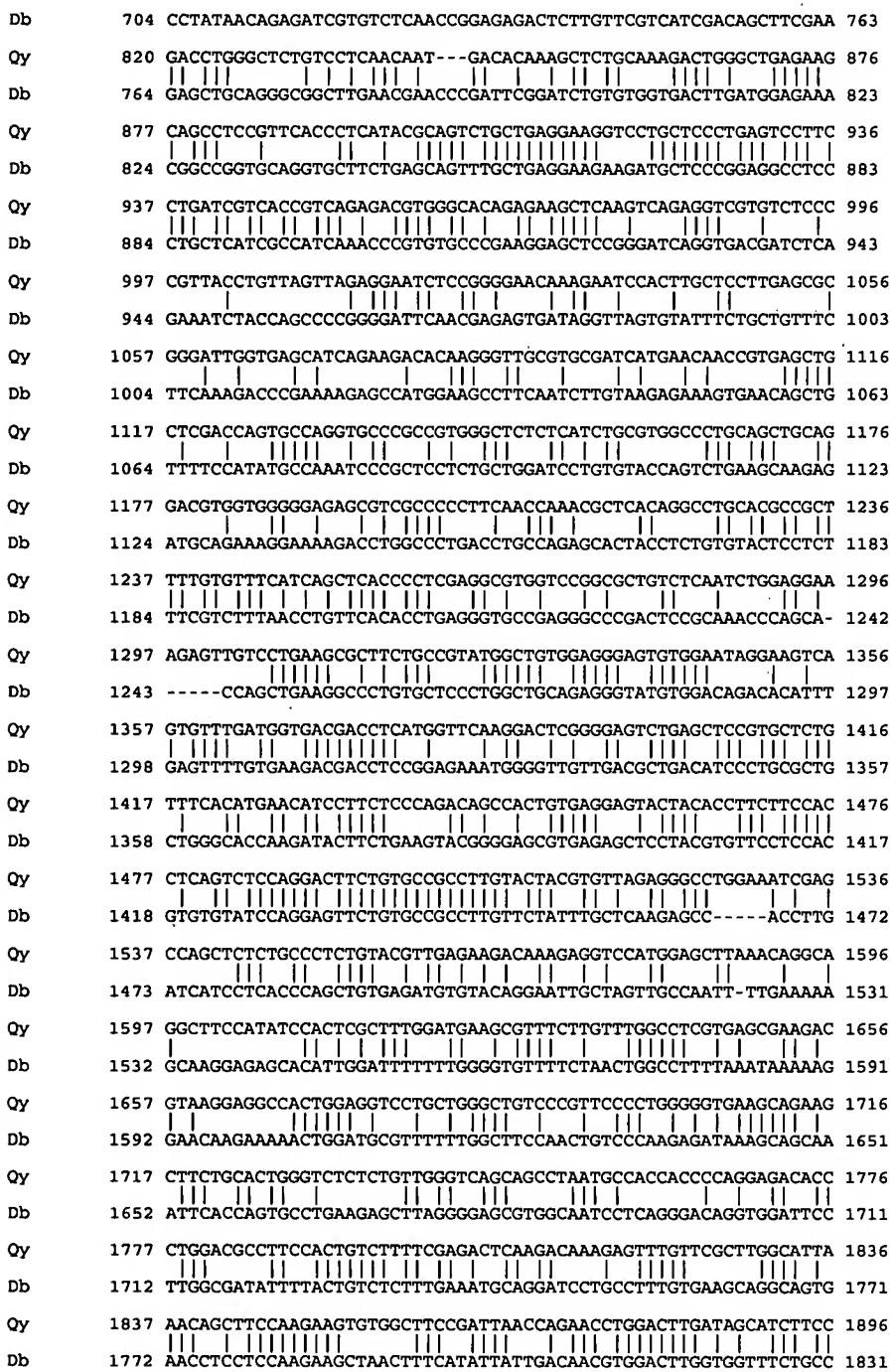
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RESULT 5
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  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Eliot Spindel
             cDNA Library Preparation: CLONTECH
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             DNA Sequencing by: Agencourt Bioscience Corporation
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ORIGIN

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Qy       2332 TCTTTGAGGCTGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATC 2391
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Db        183 TCTTTGAGGCTGGATCGCTGTGGATTGACCCACGCCTGTTACCTGAAGATCTCCCAAATC 242

Qy       2392 CTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAG 2451
             |||||||||||| |||| |||||| ||||||| ||||||||||||   ||||||||||||
Db        243 CTTACGACCTCTCCCAACCTGAAGTCTCTGATCCTGGCAGGAAATGAGGTGACAGACCAT 302

Qy       2452 GGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATA 2511
             ||||| | |||||||||||||||||||||| |||||||||||||||||||||||||||| |
Db        303 GGAGTGACGCCTCTCAGTGATGCCTTGAGGGTCTCCCAGTGCGCCCTGCAGAAGCTGACA 362

Qy       2512 CTGG-AGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAG 2570
             |||| |||||||||||||  |||||||||||| |||||||| || ||||||||||
Db        363 CTGGAAGGACTGTGGCATCATGGCCACGGGTTGCCAAAGTCTGGCCACAACCCTCGTCAG 422

Qy       2571 CAACCGGAGCTTGACACACCTGTGCCTATCCAACAA-CAGCCTGGGGAACGAAGGTGTAA 2629
             | |||||| || |||||| |||||||||| | |||| |   |  ||||| ||||| || |
Db        423 CTACCGGAACTAGACACATCTGTGCCTATTCCACAACCTATCGAGGGAAAGAAGGAGTGA 482

Qy       2630 ATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGT 2667
             | | |||||   ||| ||   | || |||  ||||||
Db        483 AACCGCTGTGATCATCAATTGAGGTTTCCCCATGTAGT 520


RESULT 6
CO814088
LOCUS       CO814088                776 bp    mRNA    linear   EST 06-AUG-2004
DEFINITION  AGENCOURT_30247088 NIH_MGC_256 Mus musculus cDNA clone
            IMAGE:30936082 5', mRNA sequence.
ACCESSION   CO814088
VERSION     CO814088.1  GI:51032714
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 776)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Kathleen Horner, Stanford University
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM1191  row: d  column: 11
            High quality sequence stop: 724.
FEATURES             Location/Qualifiers
     source          1. .776
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30936082"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_256"
                     /note="Organ: oocyte; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; cDNA was primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb
                     resulted in an average insert size of 1.2 kb. This is a
                     primarylibrary (normalized primary library is NIH_MGC_257)
                     and was constructed by Express Genomics (Frederick, MD).
                     Note: this is a NIH_MGC library"
ORIGIN

  Query Match            9.5%;  Score 381.4;  DB 7;  Length 776;
  Best Local Similarity   70.3%;  Pred. No. 1.3e-93;
  Matches  511;  Conservative    0;  Mismatches  216;  Indels    0;  Gaps    0;

Qy       2468 GTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCA 2527
             | ||||||||||||   |||   |||    ||||| ||| |||||||||| ||||||||
Db          3 GGGATGCCTTGAGTAGCTCAATGTGTCTACTGCAAAAGTTGATACTGGACAACTGTGGCC 62
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Qy       2528 TCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTGACAC 2587
Db         63 TCACACCTGCCAGCTGCCACCTTCTGGTCTCAGCCCTTTTCAGCAACCAGAACTTGACAC 122

Qy       2588 ACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGATCCA 2647
Db        123 ACCTGTGCCTGTCAAACAACAGCCTGGGGACTGAAGGAGTGCAACAGCTGTGTCAGTTCC 182

Qy       2648 TGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGACACGG 2707
Db        183 TGAGGAATCCAGAATGTGCTCTCCAGCGGCTGATACTGAATCACTGCAACATTGTAGATG 242

Qy       2708 CTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACCTGAGCC 2767
Db        243 ATGCTTATGGCTTCCTGGCAATGAGACTTGCAAACAACACAAAGCTGACCCACCTGAGCC 302

Qy       2768 TTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGAAC 2827
Db        303 TGACCATGAACCCCGTAGGGGATGGTGCAATGAAGCTACTGTGTGAAGCTTTAAAGGAAC 362

Qy       2828 CATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGTGCTGTG 2887
Db        363 CTACTTGTTACCTTCAAGAACTGGAACTAGTGGACTGCCAACTCACACAGAACTGCTGCG 422

Qy       2888 AGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCACGGACA 2947
Db        423 AGGACCTGGCCTGTATGATCACAACAACCAAGCACTTAAAAAGTTTGGATCTTGGTAACA 482

Qy       2948 ATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAACAGTG 3007
Db        483 ACGCCCTGGGTGACAAAGGAGTCATAACCCTGTGTGAGGGACTGAAGCAAAGTAGCAGCT 542

Qy       3008 TTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCACTCT 3067
Db        543 CCCTGAGGAGACTTGGGTTGGGGGCATGTAAGTTGACTTCCAATTGCTGTGAGGCATTGT 602

Qy       3068 CCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATAACTTCA 3127
Db        603 CATTGGCCATCTCTTGCAACCCTCACCTGAACAGCCTAAACCTGGTGAAGAATGACTTCA 662

Qy       3128 GTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACTTACAGA 3187
Db        663 GTACATCGGGGATGTTGAAGCTGTGCTCTGCGTTCCAATGCCCTGTCTCTAACCTGGGGA 722

Qy       3188 TAATTGG 3194
Db        723 TAATTGG 729
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RESULT 7
AK016782
LOCUS AK016782 1913 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933411P06 product:maternal effect gene, full insert sequence.
ACCESSION AK016782
VERSION AK016782.1 GI:12855702
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1913)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="taxon:10090"
/clone="4933411P06"

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                     /tissue_type="testis"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     CDS             735. .1544
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                     (MGD|MGI:1345193)
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                     HLKSLDLGNNALGDKGVITLCEGLKQSSSSLRRLGLGACELTSNCCESLSLAISCNPH
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     polyA_signal    1886. .1891
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                     /note="putative"
ORIGIN

  Query Match             9.4%;  Score 377.8;  DB 3;  Length 1913;
  Best Local Similarity   65.7%;  Pred. No. 1.8e-92;
  Matches  550;  Conservative    0;  Mismatches  287;  Indels    0;  Gaps    0;

Qy       2381 TCTCCCAAATCCTTACGACCTCCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGG 2440
Db        676 TCTGGAAGCTCCTTTTTAGCAATCAAAACTTAAAGTACCTCAATCTAGGGAACACCCCCA 735

Qy       2441 TGACAGACCAGGGAGTAATGCCTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGC 2500
Db        736 TGAAGGATGATGACATGAAGTTAGCCTGCGAAGCGCTGGAACATCCAAAGTGCGCCCTGG 795

Qy       2501 AGAAGCTGATACTGGAGGACTGTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAG 2560
Db        796 AGGCTCTGAGACTGGACAGCTGTGGCCTCACACCTGCCAGCTGCCACCTTCTGGTCTCAG 855

Qy       2561 CCCTCGTCAGCAACCGGAGCTTGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACG 2620
Db        856 CCCTTTTCAGCAACCAGAACTTGACACACCTGTGCCTGTCAAACAACAGCCTGGGGACTG 915

Qy       2621 AAGGTGTAAATCTACTGTGTCGATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGA 2680
Db        916 AAGGAGTGCAACAGCTGTGTCAGTTCCTGAGGAATCCAGAATGTGCTCTCCAGCGGCTGA 975

Qy       2681 TGCTGAATCAGTGCCACCTGGACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGG 2740
Db        976 TACTGAATCATTGCAACATTGTAGATGATGCTTATGGCTTCCTGGCATTGAGACTTGCAA 1035

Qy       2741 GTAACTCATGGCTGACGCACCTGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGA 2800
Db        1036 ACAACACAAAGCTGACCCACCTGAGCCTGACCATGAACCCCGTAGGGGATGGTGCAATGA 1095

Qy       2801 AGCTTCTGTGCGAGGTCATGAGAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAA 2860
Db        1096 AGCTACTGTGTGAAGCTTTAAAGGAACCTACTTGTTACCTTAAAGAACTGAAACTAGTGG 1155

Qy       2861 AGTGTCATCTCACCGCCGCGTGCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGAC 2920
Db        1156 ACTGCCAACTTATGCAGAACTGCTGTGAGGACCTGGCCTGTATGATCACAACAACCAAGC 1215

Qy       2921 ACCTGAAGAGCCTGGATCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGT 2980
Db        1216 ACTTAAAAAGTTTGGATCTTGGTAACAACGCCCTGGGTGACAAAGGAGTCATAACCCTGT 1275

Qy       2981 GCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGAC 3040
Db        1276 GCGAGGGACTGAAGCAAAGTAGCAGCTCCCTGAGGAGACTTGGGTTGGGGGCATGTGAGT 1335

Qy       3041 TGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCA 3100
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Qy       3101 GTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCT 3160
Db        1396 GCCTAAACCTGATGAAGAATGACTTCAGTACATCGGGGAAGTTGAAGCTGTGCTCTGCGT 1455

Qy       3161 TTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTG 3217
Db        1456 TCCAATGCCCTGTCTCTAACCTGGGGATAATTGGGTCTGGCAACTTGGGCTCACCTG 1512


RESULT 8
CO804754
LOCUS       CO804754                808 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  AGENCOURT_30257031 NIH_MGC_256 Mus musculus cDNA clone
            IMAGE:30938137 5', mRNA sequence.
ACCESSION   CO804754
VERSION     CO804754.1  GI:50992934
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 808)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Kathleen Horner, Stanford University
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM1196  row: j  column: 02
            High quality sequence stop: 742.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_256"
                     /note="Organ: oocyte; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; cDNA was primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb
                     resulted in an average insert size of 1.2 kb. This is a
                     primarylibrary (normalized primary library is NIH_MGC_257)
                     and was constructed by Express Genomics (Frederick, MD).
                     Note: this is a NIH_MGC library"
ORIGIN

  Query Match             9.3%;  Score 374.4;  DB 7;  Length 808;
  Best Local Similarity   70.0%;  Pred. No. 1.1e-91;
  Matches  504;  Conservative    0;  Mismatches  216;  Indels    0;  Gaps    0;

Qy       2462 CTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACT 2521
Db          10 CCCTTGGGAATGCCTTGAGTAGCTCAATGTGTCTACTGCAAAAGTTGATACTGGACAACT 69

Qy       2522 GTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCT 2581
Db          70 GTGGCCTCACACCTGCCAGCTGCCACCTTCTGGTCTCAGCCCTTTTCAGCAACCAGAACT 129

Qy       2582 TGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTC 2641
Db         130 TGACACACCTGTGCCTGTCAAACAACAGCCTGGGGACTGAAGGAGTGCAACAGCTGTGTC 189
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Qy       2642 GATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGG 2701
Db        190 AGTTCCTGAGGAATCCAGAATGTGCTCTCCAGCGGCTGATACTGAATCACTGCAACATTG 249

Qy       2702 ACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACC 2761
Db        250 TAGATGATGCTTATGGCTTCCTGGCAATGAGACTTGCAAACAACACAAAGCTGACCCACC 309

Qy       2762 TGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGA 2821
Db        310 TGAGCCTGACCATGAACCCCGTAGGGGATGGTGCAATGAAGCTACTGTGTGAAGCTTTAA 369

Qy       2822 GAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGT 2881
Db        370 AGGAACCTACTTGTTACCTTCAAGAACTGGAACTAGTGGACTGCCAACTCACACAGAACT 429

Qy       2882 GCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCA 2941
Db        430 GCTGCGAGGACCTGGCCTGTATGATCACAACAACCAAGCACTTAAAAAGTTTGGATCTTG 489

Qy       2942 CGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGA 3001
Db        490 GTAACAACGCCCTGGGTGACAAAGGAGTCATAACCCTGTGTGAGGGACTGAAGCAAAGTA 549

Qy       3002 ACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGG 3061
Db        550 GCAGCTCCCTGAGGAGACTTGGGTTGGGGGCATGTAAGTTGACTTCCAATTGCTGTGAGG 609

Qy       3062 CACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATA 3121
Db        610 CATTGTCATTGGCCATCTCTTGCAACCCTCACCTGAACAGCCTAAACCTGGTGAAGAATG 669

Qy       3122 ACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTAACT 3181
Db        670 ACTTCAGTACATCGGGGATGTTGAAGCTGTGCTCTGCGTTCCAATGCCCTGTCTCTAACT 729
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RESULT 9
BU634350/c
LOCUS BU634350 693 bp mRNA linear EST 23-SEP-2002
DEFINITION UI-H-FL1-bgx-m-16-0-UI.s1 NCI_CGAP_FL1 Homo sapiens cDNA clone UI-H-FL1-bgx-m-16-0-UI 3', mRNA sequence.
ACCESSION BU634350
VERSION BU634350.1 GI:23301605
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 693)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES Location/Qualifiers
source 1. .693
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FL1-bgx-m-16-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FL1"
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FL1 is a normalized cDNA library derived from a pool of mRNA obtained from 4 cell lines from grade III chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAGGTCGGTG. The cell lines were provided by Dr. James Martin from the University of Iowa.
TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG_LIB=UI-H-FL1
TAG_SEQ=GAGGTCGGTG"
ORIGIN

Query Match 8.9%; Score 358.2; DB 5; Length 693;
Best Local Similarity 98.7%; Pred. No. 3.3e-87;
Matches 371; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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Qy       2937 TCTCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCA 2996
Db        693 TCTCACGGACAATGCCCTGGGTGACGGTGGGG-TGCTGCACTGTGCGAGNGACTGAAGCA 635

Qy       2997 AAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTG 3056
Db        634 AAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTG 575

Qy       3057 TGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCA 3116
Db        574 TGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCA 515

Qy       3117 GAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTC 3176
Db        514 GAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTC 455

Qy       3177 TAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCT 3236
Db        454 TAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCT 395

Qy       3237 GGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGA 3296
Db        394 GGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGA 335

Qy       3297 TGAAGATGACCGACAC 3312
Db        334 TGAAGATGACCGGTAC 319
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RESULT 10
BU630481/c
LOCUS BU630481 684 bp mRNA linear EST 23-SEP-2002
DEFINITION UI-H-FL0-bdk-c-22-0-UI.s1 NCI_CGAP_FL0 Homo sapiens cDNA clone UI-H-FL0-bdk-c-22-0-UI 3', mRNA sequence.
ACCESSION BU630481
VERSION BU630481.1 GI:23297486
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 684)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)

```
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES            Location/Qualifiers
     source         1. .684
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="UI-H-FL0-bdk-c-22-0-UI"
                    /tissue_type="Cell lines"
                    /dev_stage="Adult"
                    /lab_host="DH10B (Life Technologies)"
                    /clone_lib="NCI_CGAP_FL0"
                    /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
                    (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                    Site_2: Not I; NCI_CGAP_FL0 is a cDNA library derived from
                    a pool of mRNA obtained from 4 cell lines from grade III
                    chondrosarcoma tissues. The library was constructed
                    according to Bonaldo, Lennon and Soares, Genome Research,
                    6:791-806, 1996. First strand cDNA synthesis was primed
                    with an oligo-dT primer containing a Not I site. Double
                    stranded cDNA was ligated to an EcoR I adaptor, digested
                    with Not I, and cloned directionally into pT7T3-Pac
                    vector. The oligonucleotide used to prime the synthesis of
                    first-strand cDNA contains a library tag sequence that is
                    located between the Not I site and the (dT)18 tail. The
                    sequence tag for this library is GAGGTCGGTG. The cell line
                    was provided by Dr James Martin from University of Iowa.
                    TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
                    TAG_LIB=UI-H-FL0
                    TAG_SEQ=GAGGTCGGTG"
ORIGIN

  Query Match             8.9%;  Score 357.2;  DB 5;  Length 684;
  Best Local Similarity   98.9%;  Pred. No. 6.1e-87;
  Matches  370;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy       2939 TCACGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAA 2998
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        684 TCACGGACAATGCCCTGGGTGACGGT-GGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAA 626

Qy       2999 AGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTG 3058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 AGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTG 566

Qy       3059 AGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGA 3118
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 AGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGA 506

Qy       3119 ATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTA 3178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        505 ATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCTTTGCCTGTCCCACGTCTA 446

Qy       3179 ACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGG 3238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 ACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGCAAATAAGGAAGCTGCTGG 386

Qy       3239 AGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTAGTTGGCATTCTTTTGATG 3298
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        385 AGGAAGTGCAGCTACTCAAGCCCCGAATCGTAATTGACGGTAGTTGGCATTCTTTTGATG 326

Qy       3299 AAGATGACCGACAC 3312
             |||||||||| ||
Db        325 AAGATGACCGGTAC 312
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RESULT 11
CO802335
LOCUS       CO802335                786 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  AGENCOURT_30254102 NIH_MGC_256 Mus musculus cDNA clone
            IMAGE:30940090 5', mRNA sequence.
ACCESSION   CO802335
VERSION     CO802335.1  GI:50990515
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 786)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Kathleen Horner, Stanford University
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM1201  row: k  column: 11
            High quality sequence stop: 505.
FEATURES            Location/Qualifiers
     source         1. .786
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="IMAGE:30940090"
                    /lab_host="DH10B TonA"
                    /clone_lib="NIH_MGC_256"
                    /note="Organ: oocyte; Vector: pExpress-1; Site_1: EcoRV;
                    Site_2: NotI; cDNA was primed using oligo-dT primer:
                    5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                    the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb
                    resulted in an average insert size of 1.2 kb. This is a
                    primarylibrary (normalized primary library is NIH_MGC_257)
                    and was constructed by Express Genomics (Frederick, MD).
                    Note: this is a NIH_MGC library"
ORIGIN

  Query Match             8.7%;  Score 349.2;  DB 7;  Length 786;
  Best Local Similarity   69.3%;  Pred. No. 1.1e-84;
  Matches  474;  Conservative    0;  Mismatches  210;  Indels    0;  Gaps    0;

Qy       2462 CTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACT 2521
             | ||  |  ||||||||||   |||  |||    ||||| ||| ||||||||||  |||
Db          1 CCCTTGGGAATGCCTTGAGTAGCTCAATGTGTCTACTGCAAAAGTTGATACTGGACAACT 60

Qy       2522 GTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCT 2581
             |||||  |||||  |  |  | |||||   |||||  |||||||||  |||||||| || ||
Db         61 GTGGCCTCACACCTGCCAGCTGCCACCTTCTGGTCTCAGCCCTTTTCAGCAACCAGAACT 120

Qy       2582 TGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTC 2641
             |||||||||||||||| || ||||||||||||||||  |||||  ||  | |  |||||||
Db         121 TGACACACCTGTGCCTGTCAAACAACAGCCTGGGGACTGAAGGAGTGCAACAGCTGTGTC 180

Qy       2642 GATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGG 2701
               | | |||||  |||  | |||  ||| ||| |||||||  |||||||| ||| || | |
Db         181 AGTTCCTGAGGAATCCAGAATGTGCTCTCCAGCGGCTGATACTGAATCACTGCAACATTG 240

Qy       2702 ACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACC 2761
                | ||  | ||| || || ||| |    |||       ||| ||  ||||||  ||||
Db         241 TAGATGATGCTTATGGCTTCCTGGCAATGAGACTTGCAAACAACACAAAGCTGACCCACC 300

Qy       2762 TGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGA 2821
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Db        301 TGAGCCTGACCATGAACCCCGTAGGGGATGGTGCAATGAAGCTACTGTGTGAAGCTTTAA 360

Qy       2822 GAGAACCATCTTGTCATCTCCAGGACCTGGAGTTGGTAAAGTGTCATCTCACCGCCGCGT 2881

Db        361 AGGAACCTACTTGTTACCTTCAAGAACTGGAACTAGTGGACTGCCAACTCACACAGAACT 420

Qy       2882 GCTGTGAGAGTCTGTCCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCA 2941

Db        421 GCTGCGAGGACCTGGCCTGTATGATCACAACAACCAAGCACTTAAAAAGTTTGGATCTTG 480

Qy       2942 CGGACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGA 3001

Db        481 GTAACAACGCCCTGGGTGACAAAGGAGTCATAACCCTGTGTGAGGGACTGAAGCAAAGTA 540

Qy       3002 ACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGG 3061

Db        541 GCAGCTCCCTGAGGAGACTTGGGTTGGGGGCATGNTAGTTGATTTCCAATTGCTGTGAGG 600

Qy       3062 CACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAACCTGGTGCAGAATA 3121

Db        601 CATTGTCATTGGCCATCTCTTGCNACCCCTCACTGAACAGCCTAAACCTGGTGAAAGATG 660

Qy       3122 ACTTCAGTCCCAAAGGAATGATGA 3145

Db        661 ACTTCAGTACATCGGGAATGTTGA 684


RESULT 12
CO382844
LOCUS       CO382844                792 bp    mRNA    linear   EST 30-JUN-2004
DEFINITION  AGENCOURT_26622956 NIH_MGC_253 Rattus norvegicus cDNA clone
            IMAGE:7303813 5', mRNA sequence.
ACCESSION   CO382844
VERSION     CO382844.1  GI:49490946
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 792)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
            College of Wisconsin
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15339  row: g  column: 11
            High quality sequence stop: 690.
FEATURES             Location/Qualifiers
     source          1. .792
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:7303813"
                     /tissue_type="Ovary - Brown Norway Line 3 Age 8 weeks.
                     Tissues were snap-frozen and transfered in -70c. RNAse
                     free the entire procedure."
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_253"
                     /note="Organ: ovary; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; RNA obtained from female animals at 8 wk
                     old. Tissues were snap-frozen and kept at -80C for two
                     days before RNA extraction and purification (Tri-reagent
                     method). cDNA was primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb
                     resulted in an average insert size of 1.5 kb. This primary
                     library is normalized (non-normalized primary library is
                     NIH_MGC_252) and was constructed by Express Genomics
                     (Frederick, MD). Note: this is a NIH_MGC library."
ORIGIN

  Query Match          8.3%;  Score 336;  DB 7;  Length 792;
  Best Local Similarity   66.6%;  Pred. No. 4.9e-81;
  Matches  480;  Conservative    0;  Mismatches  241;  Indels    0;  Gaps    0;

Qy       2102 TGACAGAGCGGGCCATGAAGACCCTGTGTGCCAAGCTGAGGCATCCCACCTGCAAGATAC 2161

Db          2 TGAATGAATGGTCCATGAAGATTCTATGCCTCAAGCTGAGGAATTCATCCTGCAGCATAC 61

Qy       2162 AGACCCTGATGTTTAGAAATGCACAGATTACCCCTGGTGTGCAGCACCTCTGGAGAATCG 2221

Db         62 AGAATCTAACGTTTAAGAATTCAGAGGTAGTTTCTGGCCTGCAATATCTCTGGATGCTCC 121

Qy       2222 TCATGGCCAACCGTAACCTAAGATCCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGG 2281

Db        122 TTGTTAGCAATCGGAACTTAAAGTACCTCAATCTAGGGAACACGCCCATGAAGGACGATG 181

Qy       2282 ATGTAAGGATGGCGTGTGAAGCCTTAAAACACCCAAAATGTTTGTTGGAGTCTTTGAGGC 2341

Db        182 ACATCAAGTTAGCCTGTGAAGCACTGAAACATCCAAGCTGTTCCCTGGAGACCCTGAGGT 241

Qy       2342 TGGATTGCTGTGGATTGACCCATGCCTGTTACCTGAAGATCTCCCAAATCCTTACGACCT 2401

Db        242 TGGATTCCTGTGAGTTAACCCTCACTGGTTATGAGCTGATCTCCAAGCTCCTTCTTTCAG 301

Qy       2402 CCCCCAGCCTGAAATCTCTGAGCCTGGCAGGAAACAAGGTGACAGACCAGGGAGTAATGC 2461

Db        302 CCAGCAGCCTAAAGTGTCTCAGCCTGGCCAGAAATAAGGTGGGGGTAAAGAGTATGACAT 361

Qy       2462 CTCTCAGTGATGCCTTGAGAGTCTCCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACT 2521

Db        362 CCCTTGGGGAAGCCTTGAGTAGCTCTACATGTACACTGCAGAAGCTGATACTGGACGGCT 421

Qy       2522 GTGGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCT 2581

Db        422 GTGACCTCATACCTGTCAGCTGCCACATGCTGACCTCCGCCCTCTCCAGCAACCGGAACT 481

Qy       2582 TGACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTC 2641

Db        482 TGACTCACCTGTGCCTGTCAAACAACAGCTTGGGGACTGAAGAAGTGCAACAGCTGTGTC 541

Qy       2642 GATCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGG 2701

Db        542 AGTTCCTGAAGAAACCAGAATGTGCTCTCCGGCGGCTGATACTGAATCATTGCAACATTA 601

Qy       2702 ACACGGCTGGCTGTGGTTTTCTTGCACTTGCGCTTATGGGTAACTCATGGCTGACGCACC 2761

Db        602 TCAAGGATGCCTACGGCTTCCTGGCGTTGATACTGGCAAACAACAGAAAGCTGACGCACC 661

Qy       2762 TGAGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGA 2821

Db        662 TGAGCCTGACCATGAACCCTGTANGAAATAGTGCAATGAAGCTACTGTGTGAAGCTTTAA 721

Qy       2822 G 2822

Db        722 G 722


RESULT 13
BM454123
LOCUS       BM454123                1119 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6419582 NCI_CGAP_Ov44 Mus musculus cDNA clone
            IMAGE:5504420 5', mRNA sequence.
```

```
ACCESSION   BM454123
VERSION     BM454123.1  GI:18503163
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1119)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Aaron Hsueh
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12145  row: l  column: 21
            High quality sequence start: 3
            High quality sequence stop: 705.
FEATURES             Location/Qualifiers
     source          1. .1119
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                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5504420"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Ov44"
                     /note="Organ: ovary, PMSG-treated; Vector: pCMV-SPORT6.1;
                     Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
                     Primer: Oligo dT. Average insert size 2.2 kb. Library
                     constructed by Life Technologies. Note: this is a NCI_CGAP
                     Library."
ORIGIN

  Query Match             8.0%;  Score 323.4;  DB 4;  Length 1119;
  Best Local Similarity   62.7%;  Pred. No. 1.7e-77;
  Matches  605;  Conservative    0;  Mismatches  346;  Indels   14;  Gaps    6;

Qy        842 ATGACACAAAGCTCTGCAAAGACTGGGCTGAGAAGCAGCCTCCGTTCACCCTCATACGCA 901
              |||| |  |  || | || |||||||   ||  | |||||     | || ||| ||   ||
Db         13 ATGATATGACACTATCCAGAGACTGGAAGGATGAACAGCCCATATACATCCTGATGTACA 72

Qy        902 GTCTGCTGAGGAAGGTCCTGCTCCCTGAGTCCTTCCTGATCGTCACCGTCAGAGACGTGG 961
              | || ||||||||||  || || ||| ||||||| || ||| | |||  |||| ||   |
Db         73 GCCTCCTGAGGAAGGCTCTCCTACCTCAGTCCTTTCTCATCATTACCACCAGAAACACAG 132

Qy        962 GCACAGAGAAGCTCAAGTCAGAGGTCGTGTCTCCCCGTTACCTGTTAGTTAGAGGAATCT 1021
              ||  ||| || |||||||||  ||| ||||| ||||  ||  |  | |||  |||| | |
Db        133 GCTTAGAAAAACTCAAGTCAATGGTTGTGTCCCCCCTCTATATACTGGTTGAAGGACTGT 192

Qy       1022 CCGGGGAACAAAGAATCCACTTGCTCCTTGAGCGCGGGATTGGTGAGCATCAGAAGACAC 1081
              | |    |   |||   ||  || |||| |||  |         ||||  | | |  | ||
Db        193 CTGCATCAAGGAGATCTCAGCTGGTCCTCGAGAACATCTCCAATGAGTCTGATAGAATAC 252

Qy       1082 AAGGGTTGCGTGCGATCATGAACAACCGTGAGCTGCTCGACCAGTGCCAGGTGCCCGCCG 1141
              |||  || | | |  | ||  | || |   ||||  | ||||| |||||||  ||| | |
Db        253 AAGTCTTCCATTCTCTGATAGAAAATCACCAGCTCTTTGACCAATGCCAGGCCCCCTCTG 312

Qy       1142 TGGGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGACGTGGTGGGGGAGAGCGTCGCCC 1201
              || |||| ||  |||| | ||| || ||||| ||| |     ||||  ||||   | |||
Db        313 TGTGCTCCCTGGTCTGTGAGGCTCTACAGCTACAGAAGAAACTGGGAAAGAGATGCACCC 372

Qy       1202 CCTTCAACCAAACGCTCACAGGCCTGCACGCCGCTTTTGTGTTTCATCAGCTCACCCCTC 1261
                |  ||| || ||||| ||  ||  | ||| | || ||||||| |||||||||
Db        373 TACCCTGCCAGACTCTCACCGGTTTGTATGCCACGTTGGTGTTTCACCAGCTCACCTTGA 432

Qy       1262 GAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCCTGAAGCGCTTCTGCC 1321
              | |     || | ||  ||||| || ||| |||    ||   ||   | | || |||
Db        433 AAAGGCCTTCCCAGAGCGCTCTCAGTCAGGAAGAACAGATTACTCTAGTGGGTTTGTGCA 492

Qy       1322 GTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTTGATGGTGACGACCTCATGG 1381
              |||| |  || |||||||||  | || ||| |||||  ||| ||| |||| | |
Db        493 TGATGGCAGCTGAAGGAGTGTGGACCATGAGGTCGGTGTTCTATGATGATGACCTGAAGA 552

Qy       1382 TTCAAGGACTCGGGGAGTCTGAGCTCCGTGCTCTGTTTCACATGAACATCCTTCTCCCAG 1441
                | | ||   |||||||||| ||   || || ||||||||||||||||||||||  |
Db        553 ACTATAGCCTAAAGGAGTCTGAGATCTTGGCCCTCTTTCACATGAACATCCTTCTCCAGG 612

Qy       1442 ACAGCC---ACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGACTTCTGTG 1498
                |||   || ||||| |||  ||    |||| |||||||||| || ||||| |||| ||
Db        613 TTGGCCACAACAGTGAGCAGTGTTATGTTTTCTCCCACCTCAGCCTGCAGGATTTCTTTG 672

Qy       1499 CCGCCTTGTACTACGTGTTAGAGGGCCTGGAAATCGAGCCAGCTCTCTGCCCTCTGTACG 1558
              | ||||| || || || ||||| || |||||     ||       ||        |  | |
Db        673 CTGCCTTATATTATGTTTTAGAAGGGCTGGA---GGAATGGAATCAGCATTTTTGCTTCA 729

Qy       1559 TTGAGAAGACAAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATATCCACTCGCTTT 1618
              |||| ||   || |||   ||||||| | |   ||  |     | | |  | |   ||
Db        730 TTGAAAACCAAAGGAGCATCATGGAGGTGA---AGAGAACTGACGACACTCGCCTTCTCG 786

Qy       1619 GGATGAAGCGTTTCTTGTTTGGCCTCGTGAGCGAAGACGTAAGGAGGCCACT-GGAGGTC 1677
              |||||||||||||||| |||||||| ||| | | ||   |    || | | || ||||||
Db        787 GGATGAAGCGTTTCTTATTTGGCCTCATGAACAAGGATATCTTGAAGACTCTGGGAGGTT 846

Qy       1678 CTGCTGGGCTGTCCCGTTCCCCTGGGGGTGAAGCAGAAGCTTCTGCACTGGGTCTCTCTG 1737
              ||| | |  | ||||||     |    |||   |   ||||| |  ||||||||||||||||
Db        847 CTGTTTGAATATCCCGTGATTCCACTGGT--TGACAAAGCTCCCACACTGGGTCTCTCTG 904

Qy       1738 TTGGGTCAGCAGCCTAATGCCACCACCCCAGGAGACACCCTGGACGCCTTCCACTGTCTT 1797
              | | ||||||| | |  ||  || ||| |   |    |||||| |||||| | || ||
Db        905 ATAGCTCAGCAGGCCATGGCACCCGCCCAA--TGGACACCTGGATGCCTTCAATTGGCTA 962

Qy       1798 TTCGA 1802
              || ||
Db        963 TTTGA 967
```

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RESULT 14
CO815646
LOCUS       CO815646                739 bp    mRNA    linear   EST 06-AUG-2004
DEFINITION  AGENCOURT_30254302 NIH_MGC_256 Mus musculus cDNA clone
            IMAGE:30939911 5', mRNA sequence.
ACCESSION   CO815646
VERSION     CO815646.1  GI:51035046
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 739)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Kathleen Horner, Stanford University
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM1201  row: c  column: 24
            High quality sequence stop: 650.
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                     Site_2: NotI; cDNA was primed using oligo-dT primer:
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                     the EcoRV/NotI sites of pExpress-1. Size-selection >0.5 kb
                     resulted in an average insert size of 1.2 kb. This is a
                     primarylibrary (normalized primary library is NIH_MGC_257)
                     and was constructed by Express Genomics (Frederick, MD).
                     Note: this is a NIH_MGC library"
ORIGIN

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  Matches  448;  Conservative    0;  Mismatches  196;  Indels    1;  Gaps    1;

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Db             1 CTTGGGAATGCCTTGAGTAGCTCAATGTGTCTACTGCAAAAGTTGATACTGGACAACTGT 60

Qy       2524 GGCATCACAGCCACGGGTTGCCAGAGTCTGGCCTCAGCCCTCGTCAGCAACCGGAGCTTG 2583
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Qy       2584 ACACACCTGTGCCTATCCAACAACAGCCTGGGGAACGAAGGTGTAAATCTACTGTGTCGA 2643
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Db           121 ACACACCTGTGCCTGTCAAACAACAGCCTGGGGACTGAAGGAGTGCAACAGCTGTGTCAG 180

Qy       2644 TCCATGAGGCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGCCACCTGGAC 2703
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Db           241 GATGATGCTTATGGCTTCCTGGCAATGAGACTTGCAAACAACACAAAGCTGACCCACCTG 300

Qy       2764 AGCCTTAGCATGAACCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGA 2823
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Db           301 AGCCTGACCATGAACCCCGTAGGGGATGGTGCAATGAAGCTACTGTGTGAAGCTTTAAAG 360

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Db           421 TGCGAGGACCTGGCCTGTATGATCACAACAACCAAGCACTTAAAAAGTTTGGATCTTGGT 480

Qy       2944 GACAATGCCCTGGGTGACGGTGGGGTTGCTGCGCTGTGCGAGGGACTGAAGCAAAAGAAC 3003
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Db           481 AACAACGCCCTGGGTGACAAAGGAGTCATAACCCTGTGTGAGGGACTGAAGCAAAGTAGC 540

Qy       3004 AGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATTGCTGTGAGGCA 3063
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Db           541 AGCTCCCTGAGGAGACTTGGGTTGGGGGCATGTAAGTTGACTTCCAATTGCTGTGAGGCA 600

Qy       3064 CTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCAGTCTAAAC 3108
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Db           601 TTGTCATTGGCCATCTCTTG-AACCCTCACCTGAACAGCCTNACC 644


RESULT 15
BU618831/c
LOCUS       BU618831                642 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  UI-H-FH1-bfl-i-19-0-UI.s1 NCI_CGAP_FH1 Homo sapiens cDNA clone
            UI-H-FH1-bfl-i-19-0-UI 3', mRNA sequence.
ACCESSION   BU618831
VERSION     BU618831.1  GI:23285046
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 642)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
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                     /clone_lib="NCI_CGAP_FH1"
                     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_FH1 is a normalized cDNA library
                     obtained from a cell line derived from grade I
                     chondrosarcoma tissue. The library was constructed and
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     AGAATCCGGC. The cell line was provided by Dr. James Martin
                     from the University of Iowa.
                     TAG_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1
                     Chondrosarcoma
                     TAG_LIB=UI-H-FH1
                     TAG_SEQ=AGAATCCGGC"
ORIGIN

  Query Match             7.8%;  Score 313.6;  DB 5;  Length 642;
  Best Local Similarity   98.5%;  Pred. No. 7.3e-75;
  Matches  327;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy       2981 GCGAGGGACTGAAGCAAAAGAACAGTGTTCTGACGAGACTCGGGTTGAAGGCATGTGGAC 3040
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Db            642 GCGAGGGACTGAAGCAAAAGAACAGTG-TCTGACGAGACTCGGGTTGAAGGCATGTGGAC 584

Qy       3041 TGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCA 3100
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Db            583 TGACTTCTGATTGCTGTGAGGCACTCTCCTTGGCCCTTTCCTGCAACCGGCATCTGACCA 524

Qy       3101 GTCTAAACCTGGTGCAGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCGGCCT 3160
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Qy       3161 TTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGC 3220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            463 TTGCCTGTCCCACGTCTAACTTACAGATAATTGGGCTGTGGAAATGGCAGTACCCTGTGC 404

Qy       3221 AAATAAGGAAGCTGCTGGAGGAAGTGCAGCTACTCAAGCCCCGAGTCGTAATTGACGGTA 3280
                ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
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Qy       3281 GTTGGCATTCTTTTGATGAAGATGACCGACAC 3312
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Db        343 TTTGGCATTCTTTTGATGAAGATGACCGGTAC 312
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GenCore version 5.1.6

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Perfect score: 1344
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	9	0.7	209	4	US-09-388-221B-19	Sequence 19, Appl
2	9	0.7	1399	4	US-09-388-221B-4	Sequence 4, Appli
3	9	0.7	1424	4	US-09-388-221B-12	Sequence 12, Appl
4	9	0.7	1443	4	US-09-388-221B-6	Sequence 6, Appli
5	9	0.7	1454	4	US-09-388-221B-10	Sequence 10, Appl
6	9	0.7	1473	4	US-09-388-221B-2	Sequence 2, Appli
7	8	0.6	150	4	US-09-270-767-32603	Sequence 32603, A
8	8	0.6	150	4	US-09-270-767-47820	Sequence 47820, A
9	8	0.6	296	4	US-09-252-991A-22293	Sequence 22293, A
10	8	0.6	321	4	US-09-902-540-10274	Sequence 10274, A
11	8	0.6	376	4	US-09-902-540-9957	Sequence 9957, Ap
12	8	0.6	388	4	US-09-248-796A-17824	Sequence 17824, A
13	8	0.6	661	4	US-09-371-338-7	Sequence 7, Appli
14	7	0.5	59	4	US-09-270-767-57972	Sequence 57972, A
15	7	0.5	60	4	US-09-543-681A-4574	Sequence 4574, Ap
16	7	0.5	60	4	US-09-513-999C-7527	Sequence 7527, Ap
17	7	0.5	63	4	US-09-513-999C-6481	Sequence 6481, Ap
18	7	0.5	94	4	US-09-270-767-59952	Sequence 59952, A
19	7	0.5	108	4	US-09-216-393B-4	Sequence 4, Appli
20	7	0.5	110	4	US-09-543-681A-6458	Sequence 6458, Ap
21	7	0.5	111	4	US-09-621-976-7083	Sequence 7083, Ap
22	7	0.5	117	4	US-10-101-464A-782	Sequence 782, App
23	7	0.5	118	4	US-09-270-767-41140	Sequence 41140, A
24	7	0.5	118	4	US-09-270-767-56356	Sequence 56356, A
25	7	0.5	126	4	US-09-640-211A-2108	Sequence 2108, Ap
26	7	0.5	128	4	US-09-732-210-647	Sequence 647, App
27	7	0.5	128	4	US-09-513-999C-7418	Sequence 7418, Ap
28	7	0.5	130	4	US-10-101-464A-780	Sequence 780, App
29	7	0.5	151	4	US-09-270-767-33903	Sequence 33903, A
30	7	0.5	174	4	US-09-270-767-44506	Sequence 44506, A
31	7	0.5	176	4	US-09-270-767-32581	Sequence 32581, A
32	7	0.5	176	4	US-09-270-767-47798	Sequence 47798, A
33	7	0.5	180	4	US-09-489-039A-9331	Sequence 9331, Ap
34	7	0.5	183	4	US-09-489-039A-7626	Sequence 7626, Ap
35	7	0.5	187	4	US-09-716-129-58	Sequence 58, Appl
36	7	0.5	189	3	US-08-779-764A-28	Sequence 28, Appl
37	7	0.5	189	3	US-08-779-764A-29	Sequence 29, Appl
38	7	0.5	189	3	US-08-779-764A-30	Sequence 30, Appl
39	7	0.5	189	4	US-09-563-456-28	Sequence 28, Appl
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41	7	0.5	189	4	US-09-563-456-30	Sequence 30, Appl
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43	7	0.5	220	4	US-09-902-540-12909	Sequence 12909, A
44	7	0.5	221	4	US-09-489-039A-12495	Sequence 12495, A
45	7	0.5	231	4	US-09-489-039A-8999	Sequence 8999, Ap

ALIGNMENTS

RESULT 1
US-09-388-221B-19
; Sequence 19, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-388-221B-19

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Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 SRPERLLFI 268
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Db 72 SRPERLLFI 80

RESULT 2
US-09-388-221B-4
; Sequence 4, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
; FILE REFERENCE: P-LJ 3650
; CURRENT APPLICATION NUMBER: US/09/388,221B
; CURRENT FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-388-221B-4

Query Match 0.7%; Score 9; DB 4; Length 1399;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 SRPERLLFI 268

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Db        400 SRPERLLFI 408


RESULT 3
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; Sequence 12, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;    LENGTH: 1424
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic Construct
US-09-388-221B-12

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Qy        260 SRPERLLFI 268
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Db        400 SRPERLLFI 408


RESULT 4
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; Sequence 6, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;    LENGTH: 1443
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-388-221B-6

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Qy        260 SRPERLLFI 268
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Db        400 SRPERLLFI 408


RESULT 5
US-09-388-221B-10
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; Patent No. 6818750
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;    LENGTH: 1454
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic Construct
US-09-388-221B-10

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Db        400 SRPERLLFI 408


RESULT 6
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; Sequence 2, Application US/09388221B
; Patent No. 6818750
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  TITLE OF INVENTION: No. 6818750el Card Proteins Involved in Cell Death Regulation
;  FILE REFERENCE: P-LJ 3650
;  CURRENT APPLICATION NUMBER: US/09/388,221B
;  CURRENT FILING DATE:  1999-09-01
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;    LENGTH: 1473
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-388-221B-2

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  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        260 SRPERLLFI 268
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Db        400 SRPERLLFI 408


RESULT 7
US-09-270-767-32603
; Sequence 32603, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32603
;    LENGTH: 150
;    TYPE: PRT
;    ORGANISM: Drosophila melanogaster
US-09-270-767-32603

  Query Match             0.6%;  Score 8;  DB 4;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 29;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1197 AELEGLGS 1204
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Db        100 AELEGLGS 107


RESULT 8
US-09-270-767-47820
; Sequence 47820, Application US/09270767
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; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47820
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47820

Query Match 0.6%; Score 8; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1197 AELEGLGS 1204
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Db 100 AELEGLGS 107

RESULT 9
US-09-252-991A-22293
; Sequence 22293, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22293
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22293

Query Match 0.6%; Score 8; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 849 QSLASALV 856
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Db 106 QSLASALV 113

RESULT 10
US-09-902-540-10274
; Sequence 10274, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10274
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10274

Query Match 0.6%; Score 8; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 GKSGIGKS 201
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Db 158 GKSGIGKS 165

RESULT 11
US-09-902-540-9957
; Sequence 9957, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9957
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-9957

Query Match 0.6%; Score 8; DB 4; Length 376;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 554 RRPLEVLL 561
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Db 120 RRPLEVLL 127

RESULT 12
US-09-248-796A-17824
; Sequence 17824, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17824
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17824

Query Match 0.6%; Score 8; DB 4; Length 388;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 302 LLRKVLLP 309
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Db 47 LLRKVLLP 54

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RESULT 13
US-09-371-338-7
; Sequence 7, Application US/09371338
; Patent No. 6613959
; GENERAL INFORMATION:
;  APPLICANT:  Sheen, Jen
;  APPLICANT:  Kovtun, Yelena V.
;  APPLICANT:  Chiu, Wan-Ling
;  TITLE OF INVENTION:  TRANSGENIC PLANTS EXPRESSING A MAPKKK
;  TITLE OF INVENTION:  PROTEIN KINASE DOMAIN
;  FILE REFERENCE:  00786/366002
;  CURRENT APPLICATION NUMBER: US/09/371,338
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER:  60/095,938
;  PRIOR FILING DATE:  1998-08-10
;  NUMBER OF SEQ ID NOS:  22
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 7
;   LENGTH: 661
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-09-371-338-7

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Db        337 DLGSVLNN 344


RESULT 14
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; Sequence 57972, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57972
;   LENGTH: 59
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-57972

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  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        475 MNILLPD 481
              |||||||
Db         53 MNILLPD 59


RESULT 15
US-09-543-681A-4574
; Sequence 4574, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4574
;   LENGTH: 60
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-4574

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         44 LKSLSLA 50


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Job time : 35 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 19, 2005, 12:11:18 ; Search time 124 Seconds
(without alignments)
4207.459 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 1736639 seqs, 388188149 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1344	100.0	1344	14	US-10-124-498-6	Sequence 6, Appli
2	1344	100.0	1344	14	US-10-066-521-6	Sequence 6, Appli
3	1006	74.9	1162	14	US-10-216-645-2	Sequence 2, Appli
4	1006	74.9	1162	15	US-10-416-642-1	Sequence 1, Appli
5	988	73.5	1143	14	US-10-216-645-4	Sequence 4, Appli
6	968	72.0	1033	15	US-10-092-900A-348	Sequence 348, App
7	602	44.8	1200	15	US-10-399-443-24	Sequence 24, Appl
8	602	44.8	1200	15	US-10-677-943-24	Sequence 24, Appl
9	602	44.8	1200	16	US-10-860-761-4	Sequence 4, Appli
10	544	40.5	682	15	US-10-407-866-96	Sequence 96, Appl
11	158	11.8	385	15	US-10-399-443-2	Sequence 2, Appli
12	158	11.8	385	15	US-10-677-943-2	Sequence 2, Appli
13	149	11.1	258	15	US-10-399-443-4	Sequence 4, Appli
14	149	11.1	258	15	US-10-677-943-4	Sequence 4, Appli
15	12	0.9	190	10	US-09-965-621-63	Sequence 63, Appl
16	12	0.9	190	15	US-10-407-866-63	Sequence 63, Appl
17	12	0.9	190	16	US-10-781-294-63	Sequence 63, Appl
18	12	0.9	321	15	US-10-407-866-116	Sequence 116, App
19	12	0.9	449	14	US-10-028-374-2	Sequence 2, Appli
20	12	0.9	449	14	US-10-183-770-2	Sequence 2, Appli
21	12	0.9	635	15	US-10-407-866-90	Sequence 90, Appl
22	12	0.9	1004	15	US-10-108-260A-3161	Sequence 3161, Ap
23	12	0.9	1027	15	US-10-407-866-68	Sequence 68, Appl
24	12	0.9	1035	10	US-09-965-621-24	Sequence 24, Appl
25	12	0.9	1035	15	US-10-407-866-24	Sequence 24, Appl
26	12	0.9	1035	16	US-10-781-294-24	Sequence 24, Appl
27	12	0.9	1061	14	US-10-124-498-18	Sequence 18, Appl
28	12	0.9	1061	14	US-10-066-521-18	Sequence 18, Appl
29	12	0.9	1111	14	US-10-216-645-5	Sequence 5, Appli
30	12	0.9	1111	15	US-10-399-443-6	Sequence 6, Appli
31	12	0.9	1111	15	US-10-677-943-6	Sequence 6, Appli
32	9	0.7	80	14	US-10-029-386-29387	Sequence 29387, A
33	9	0.7	87	16	US-10-425-115-257211	Sequence 257211,
34	9	0.7	162	9	US-09-864-761-34582	Sequence 34582, A
35	9	0.7	192	10	US-09-764-891-4432	Sequence 4432, Ap
36	9	0.7	224	17	US-10-732-923-13890	Sequence 13890, A
37	9	0.7	284	15	US-10-424-599-223227	Sequence 223227,
38	9	0.7	303	14	US-10-306-762-114	Sequence 114, App
39	9	0.7	764	15	US-10-407-866-92	Sequence 92, Appl
40	9	0.7	1399	9	US-09-388-221-4	Sequence 4, Appli
41	9	0.7	1424	9	US-09-388-221-12	Sequence 12, Appl
42	9	0.7	1429	9	US-09-996-617-2	Sequence 2, Appli
43	9	0.7	1429	9	US-09-931-071-2	Sequence 2, Appli
44	9	0.7	1429	14	US-10-029-347-3	Sequence 3, Appli
45	9	0.7	1429	14	US-10-029-347-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-124-498-6
; Sequence 6, Application US/10124498
; Publication No. US20030017983A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-367001
; CURRENT APPLICATION NUMBER: US/10/124,498
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 10/066,521
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-124-498-6

Query Match 100.0%; Score 1344; DB 14; Length 1344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         181 DRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSV 240
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Qy         901 DTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAA 960
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 2
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; Sequence 6, Application US/10066521
; Publication No. US20030027757A1
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; APPLICANT: Wang, Weiye
; APPLICANT: Blatcher, Maria
; TITLE OF INVENTION: NOVEL MOLECULES OF THE PYRIN/NBS/LRR
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 07334-334001
; CURRENT APPLICATION NUMBER: US/10/066,521
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/318,645
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/265,231
; PRIOR FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-066-521-6

Query Match 100.0%; Score 1344; DB 14; Length 1344;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db           1 MEGDKSLTFSSYGLQWCLYELDKEEFQTFKELLKKKSSESTTCSIPQFEIENANVECLAL 60

Qy          61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQAMEQEGATAAETEEQEISQA 120
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Db          61 LLHEYYGASLAWATSISIFENMNLRTLSEKARDDMKKISQAMEQEGATAAETEEQEISQA 120

Qy         121 MEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDS 180
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Qy         241 TEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIR 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 TEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIR 300

Qy         301 SLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 SLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKT 360

Qy         361 QGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTP 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 QGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTP 420
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Qy        421 RGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLP 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 RGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLP 480

Qy        481 DSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLW 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 DSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLW 540

Qy        541 MKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLF 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 MKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLF 600

Qy        601 ETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEA 660

Qy        661 CPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKI 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKI 720

Qy        721 QTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLR 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 QTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLR 780

Qy        781 LDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILED 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 LDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILED 840

Qy        841 CGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHL 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHL 900

Qy        901 DTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 DTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAA 960

Qy        961 CCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCE 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCE 1020

Qy       1021 ALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLE 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ALSLALSCNRHLTSLNLVQNNPSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLE 1080

Qy       1081 EVQLLKPRVVIDGSWHSFDEDDRHKIGLTFRLPESRAWPCALLWGMNPEQKKRVSLLAGD 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 EVQLLKPRVVIDGSWHSFDEDDRHKIGLTFRLPESRAWPCALLWGMNPEQKKRVSLLAGD 1140

Qy       1141 FKSSTRFAKSLCLATANGESQRVDNVEQSSPQPMAGTEHKQDKMLSVGYSGAWSETAELE 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 FKSSTRFAKSLCLATANGESQRVDNVEQSSPQPMAGTEHKQDKMLSVGYSGAWSETAELE 1200

Qy       1201 GLGSNSADHDHGGMAWSLGRELSSRGLCPTVLMTTAVCPGHWERLGSRGWCLNSADDHSG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GLGSNSADHDHGGMAWSLGRELSSRGLCPTVLMTTAVCPGHWERLGSRGWCLNSADDHSG 1260

Qy       1261 VSWSLGAAGLEGLVSNSADDHSGVAWSLGAAGLEGLVSNSADDHSGVSWSLGAAGLEGLV 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 VSWSLGAAGLEGLVSNSADDHSGVAWSLGAAGLEGLVSNSADDHSGVSWSLGAAGLEGLV 1320

Qy       1321 SNSADDHSGVSWSLGAAGLEGLVS 1344
              ||||||||||||||||||||||||
Db       1321 SNSADDHSGVSWSLGAAGLEGLVS 1344
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RESULT 3
US-10-216-645-2
; Sequence 2, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
; APPLICANT: WEISS, BERTRAM
; APPLICANT: LESSL, MONIKA
; APPLICANT: PETERS-KOTTIG, MICHAELE
; APPLICANT: BECKMANN, GEORG
; TITLE OF INVENTION: HUMAN MATER PROTEINS
; FILE REFERENCE: SCH-1910
; CURRENT APPLICATION NUMBER: US/10/216,645
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-216-645-2

Query Match 74.9%; Score 1006; DB 14; Length 1162;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1006; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         98 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 211

Qy        158 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 271

Qy        218 QGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 QGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 331

Qy        278 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 391

Qy        338 RGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGE 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 RGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGE 451

Qy        398 SVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 SVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 511

Qy        458 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 571

Qy        518 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 631

Qy        578 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 691

Qy        638 CPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLG 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 CPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLG 751

Qy        698 SSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHL 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 SSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHL 811

Qy        758 KEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQ 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 KEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQ 871

Qy        818 GVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVN 877
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 GVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVN 931

Qy        878 LLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLC 937
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 LLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLC 991

Qy        938 EVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGL 997
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        992 EVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGL 1051

Qy        998 KQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACP 1057
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1052 KQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACP 1111

Qy       1058 TSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDR 1103
                 ||||||||||||||||||||||||||||||||||||||||||||||
Db       1112 TSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDR 1157


RESULT 4
US-10-416-642-1
; Sequence 1, Application US/10416642
; Publication No. US20040043452A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  ARVIZU, Chandra
;  TITLE OF INVENTION: EMBRYOGENESIS ASSOCIATED PROTEINS
;  FILE REFERENCE: PF-0842 PCT
;  CURRENT APPLICATION NUMBER: US/10/416,642
;  CURRENT FILING DATE:  2003-05-13
;  PRIOR APPLICATION NUMBER: 60/249,407
;  PRIOR FILING DATE: 2000-11-15
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 1162
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040043452A1 7474830CD1
US-10-416-642-1

  Query Match             74.9%;  Score 1006;  DB 15;  Length 1162;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1006;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         98 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 157
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 211

Qy        158 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 217
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 271

Qy        218 QGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 277
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 QGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 331

Qy        278 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 337
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 391

Qy        338 RGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGE 397
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 RGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGE 451

Qy        398 SVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 457
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 SVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 511

Qy        458 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 517
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 571

Qy        518 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 577
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 631

Qy        578 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 637
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 691

Qy        638 CPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLG 697
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 CPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLG 751

Qy        698 SSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHL 757
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 SSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHL 811

Qy        758 KEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQ 817
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 KEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQ 871

Qy        818 GVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVN 877
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 GVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVN 931

Qy        878 LLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLC 937
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 LLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLC 991

Qy        938 EVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGL 997
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        992 EVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGL 1051

Qy        998 KQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACP 1057
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1052 KQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACP 1111

Qy       1058 TSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDR 1103
                 ||||||||||||||||||||||||||||||||||||||||||||||
Db       1112 TSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDR 1157


RESULT 5
US-10-216-645-4
; Sequence 4, Application US/10216645
; Publication No. US20030125282A1
; GENERAL INFORMATION:
;  APPLICANT: WEISS, BERTRAM
;  APPLICANT:  LESSL, MONIKA
;  APPLICANT:  PETERS-KOTTIG, MICHAELE
;  APPLICANT:  BECKMANN, GEORG
;  TITLE OF INVENTION: HUMAN MATER PROTEINS
;  FILE REFERENCE: SCH-1910
;  CURRENT APPLICATION NUMBER: US/10/216,645
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: DE 101 39 874.3 41
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 1143
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-216-645-4

  Query Match             73.5%;  Score 988;  DB 14;  Length 1143;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  988;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        116 EISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLA 175
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 EISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLA 210

Qy        176 GAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRK 235
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Db        211 GAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRK 270

Qy        236 KESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPP 295
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 KESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPP 330

Qy        296 FTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIG 355
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 FTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIG 390

Qy        356 EHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVF 415
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 EHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVF 450

Qy        416 HQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHM 475
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 HQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHM 510

Qy        476 NILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFH 535
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 NILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFH 570

Qy        536 IHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDA 595
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 IHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDA 630

Qy        596 FHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRD 655
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 FHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRD 690

Qy        656 ESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRH 715
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 ESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRH 750

Qy        716 PTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCL 775
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 PTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCL 810

Qy        776 LESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQK 835
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 LESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQK 870

Qy        836 LILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLML 895
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 LILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLML 930

Qy        896 NQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKC 955
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 NQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKC 990

Qy        956 HLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLT 1015
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 HLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLT 1050

Qy       1016 SDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQI 1075
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1051 SDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQI 1110

Qy       1076 RKLLEEVQLLKPRVVIDGSWHSFDEDDR 1103
                ||||||||||||||||||||||||||||
Db       1111 RKLLEEVQLLKPRVVIDGSWHSFDEDDR 1138


RESULT 6
US-10-092-900A-348
; Sequence 348, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Taupier Jr., Raymond J.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Li, Li
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Ji, Weizhen
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Vernet, Corine A.M.
;  APPLICANT:  Guo, Xiaojia Sasha
;  APPLICANT:  Tchernev,, Velizar T.
;  APPLICANT:  Fernandes, Elma R.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Liu, Yi
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Spaderna, Steven K.
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Leite, Mario W.
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Alsobrook, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-290C
;  CURRENT APPLICATION NUMBER: US/10/092,900A
;  CURRENT FILING DATE:  2002-03-07
;  PRIOR APPLICATION NUMBER: USSN 60/274,322
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/283,675
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: USSN 60/338,092
;  PRIOR FILING DATE: 2001-12-03
;  PRIOR APPLICATION NUMBER: USSN 60/274,281
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/274,191
;  PRIOR FILING DATE: 2001-03-08
;  PRIOR APPLICATION NUMBER: USSN 60/325,681
;  PRIOR FILING DATE: 2001-09-27
;  PRIOR APPLICATION NUMBER: USSN 60/304,354
;  PRIOR FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: USSN 60/279,995
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: USSN 60/294,899
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: USSN 60/287,424
;  PRIOR FILING DATE: 2001-04-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 348
;   LENGTH: 1033
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-092-900A-348

  Query Match             72.0%;  Score 968;  DB 15;  Length 1033;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  968;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        136 HGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGK 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HGGDTWDYKSHVMTKFAEEEDVRRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGK 120

Qy        196 SGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPV 255
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SGIGKSALARRIVLCWAQGGLYQGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPV 180

Qy        256 TEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIV 315
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 TEIMSRPERLLFIIDGFDDLGSVLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIV 240

Qy        316 TVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQ 375

Db        241 TVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQ 300

Qy        376 CQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVV 435

Db        301 CQVPAVGSLICVALQLQDVVGESVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVV 360

Qy        436 LKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSL 495

Db        361 LKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSL 420

Qy        496 QDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRR 555

Db        421 QDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRR 480

Qy        556 PLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSF 615

Db        481 PLEVLLGCPVPLGVKQKLLHWVSLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSF 540

Qy        616 QEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIE 675

Db        541 QEVWLPINQNLDLIASSFCLQHCPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIE 600

Qy        676 EQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQ 735

Db        601 EQWEDFCSMLGTHPHLRQLDLGSSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQ 660

Qy        736 HLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKIS 795

Db        661 HLWRIVMANRNLRSLNLGGTHLKEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKIS 720

Qy        796 QILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASAL 855

Db        721 QILTTSPSLKSLSLAGNKVTDQGVMPLSDALRVSQCALQKLILEDCGITATGCQSLASAL 780

Qy        856 VSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGN 915

Db        781 VSNRSLTHLCLSNNSLGNEGVNLLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGN 840

Qy        916 SWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHL 975

Db        841 SWLTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHL 900

Qy        976 KSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSL 1035

Db        901 KSLDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSL 960

Qy       1036 NLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSW 1095

Db        961 NLVQNNFSPKGMMKLCSAFACPTSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSW 1020

Qy       1096 HSFDEDDR 1103

Db       1021 HSFDEDDR 1028


RESULT 7
US-10-399-443-24
; Sequence 24, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute
;  APPLICANT:  Health
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
;   LENGTH: 1200
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-399-443-24

  Query Match          44.8%;  Score 602;  DB 15;  Length 1200;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1002;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         98 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 157

Db        190 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 249

Qy        158 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 217

Db        250 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 309

Qy        218 QGMFSYVPFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 277

Db        310 QGMFSYVPFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 369

Qy        278 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 337

Db        370 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 429

Qy        338 RGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGE 397

Db        430 RGISGEQRIHLLLERGIGEHQKTQGLRAIINNRELLDQCQVPAVGSLICVALQLQDVVGE 489

Qy        398 SVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 457

Db        490 SVAPFNQTLTGLHAAFAFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 549

Qy        458 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 517

Db        550 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 609

Qy        518 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 577

Db        610 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 669

Qy        578 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 637

Db        670 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 729

Qy        638 CPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLG 697

Db        730 CPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLG 789

Qy        698 SSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHL 757

Db        790 SSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHL 849

Qy        758 KEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQ 817

Db        850 KEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQ 909

Qy        818 GVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVN 877

Db        910 GVTPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVN 969

Qy        878 LLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLC 937

Db        970 LLCRSMRLPHCSLQRLMLNQCHLDTAGCGSLALALMGNSWLTHLSLSMNPVEDNGVKLLC 1029
```

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Qy        938 EVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGL 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 EVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGL 1089

Qy        998 KQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACP 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 KQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACP 1149

Qy       1058 TSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDR 1103
              |||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 TSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDR 1195
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RESULT 8
US-10-677-943-24
; Sequence 24, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; APPLICANT: represented by the Secretary of the Department of Health and
; APPLICANT: Human Services
; APPLICANT: Nelson, Lawrence
; APPLICANT: Tong, Zhi-Bin
; TITLE OF INVENTION: Human Gene Critical to Fertility
; FILE REFERENCE: 4239-64790
; CURRENT APPLICATION NUMBER: US/10/677,943
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 60/241,510
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: PCT/US02/09776
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/US01/10981
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 1200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-677-943-24

Query Match 44.8%; Score 602; DB 15; Length 1200;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1002; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy         98 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 249

Qy        158 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 309

Qy        218 QGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 QGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 369

Qy        278 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 429

Qy        338 RGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGE 397
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        430 RGISGEQRIHLLLERGIGEHQKTQGLRAIINNRELLDQCQVPAVGSLICVALQLQDVVGE 489

Qy        398 SVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 457
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        490 SVAPFNQTLTGLHAAFAFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 549

Qy        458 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 609

Qy        518 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 669

Qy        578 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 729

Qy        638 CPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLG 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 CPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLG 789

Qy        698 SSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHL 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 SSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHL 849

Qy        758 KEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQ 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 KEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQ 909

Qy        818 GVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVN 877
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 GVTPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVN 969

Qy        878 LLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLC 937
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        970 LLCRSMRLPHCSLQRLMLNQCHLDTAGCGSLALALMGNSWLTHLSLSMNPVEDNGVKLLC 1029

Qy        938 EVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGL 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 EVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGL 1089

Qy        998 KQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACP 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 KQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACP 1149

Qy       1058 TSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDR 1103
              |||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 TSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDR 1195
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RESULT 9
US-10-860-761-4
; Sequence 4, Application US/10860761
; Publication No. US20040248775A1
; GENERAL INFORMATION:
; APPLICANT: WYETH
; TITLE OF INVENTION: METHODS FOR SCREENING INHIBITORS OF APOPTOSIS
; FILE REFERENCE: AM101318
; CURRENT APPLICATION NUMBER: US/10/860,761
; CURRENT FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-860-761-4

Query Match 44.8%; Score 602; DB 16; Length 1200;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1002; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy         98 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 157
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Db        190 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 249

Qy        158 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 309

Qy        218 QGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 277
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Db        310 QGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 369

Qy        278 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 429

Qy        338 RGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGE 397
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        430 RGISGEQRIHLLLERGIGEHQKTQGLRAIINNRELLDQCQVPAVGSLICVALQLQDVVGE 489

Qy        398 SVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 457
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db        490 SVAPFNQTLTGLHAAFAFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 549

Qy        458 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 609

Qy        518 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 669

Qy        578 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 729

Qy        638 CPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLG 697
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 CPYLRKIRVDVKGIFPRDESAEACPVVPLWMRDKTLIEEQWEDFCSMLGTHPHLRQLDLG 789

Qy        698 SSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHL 757
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 SSILTERAMKTLCAKLRHPTCKIQTLMFRNAQITPGVQHLWRIVMANRNLRSLNLGGTHL 849

Qy        758 KEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQ 817
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 KEEDVRMACEALKHPKCLLESLRLDCCGLTHACYLKISQILTTSPSLKSLSLAGNKVTDQ 909

Qy        818 GVMPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVN 877
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 GVTPLSDALRVSQCALQKLILEDCGITATGCQSLASALVSNRSLTHLCLSNNSLGNEGVN 969

Qy        878 LLCRSMRLPHCSLQRLMLNQCHLDTAGCGFLALALMGNSWLTHLSLSMNPVEDNGVKLLC 937
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        970 LLCRSMRLPHCSLQRLMLNQCHLDTAGCGSLALALMGNSWLTHLSLSMNPVEDNGVKLLC 1029

Qy        938 EVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGL 997
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 EVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKSLDLTDNALGDGGVAALCEGL 1089

Qy        998 KQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACP 1057
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 KQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMKLCSAFACP 1149

Qy       1058 TSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDR 1103
              ||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 TSNLQIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWHSFDEDDR 1195

RESULT 10
US-10-407-866-96
; Sequence 96, Application US/10407866
; Publication No. US20040002593A1
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  APPLICANT:  Godzik, Adam
;  TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
;  TITLE OF INVENTION:  Encoding Nucleic Acids, and Methods of Use
;  FILE REFERENCE: 66654-10(LJ 5755)
;  CURRENT APPLICATION NUMBER: US/10/407,866
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/370,538
;  PRIOR FILING DATE: 2002-04-04
;  NUMBER OF SEQ ID NOS: 129
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
;   LENGTH: 682
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-407-866-96

  Query Match             40.5%;  Score 544;  DB 15;  Length 682;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  544;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         98 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 ISQAMEQEGATAAETEEQEISQAMEQEGATAAETEEQGHGGDTWDYKSHVMTKFAEEEDV 198

Qy        158 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 RRSFENTAADWPEMQTLAGAFDSDRWGFRPRTVVLHGKSGIGKSALARRIVLCWAQGGLY 258

Qy        218 QGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 QGMFSYVFFLPVREMQRKKESSVTEFISREWPDSQAPVTEIMSRPERLLFIIDGFDDLGS 318

Qy        278 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 VLNNDTKLCKDWAEKQPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLV 378

Qy        338 RGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGE 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 RGISGEQRIHLLLERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGE 438

Qy        398 SVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 457
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 SVAPFNQTLTGLHAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGD 498

Qy        458 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 517
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 DLMVQGLGESELRALFHMNILLPDSHCEEYYTFFHLSLQDFCAALYYVLEGLEIEPALCP 558

Qy        518 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 LYVEKTKRSMELKQAGFHIHSLWMKRFLFGLVSEDVRRPLEVLLGCPVPLGVKQKLLHWV 618

Qy        578 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 637
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 SLLGQQPNATTPGDTLDAFHCLFETQDKEFVRLALNSFQEVWLPINQNLDLIASSFCLQH 678

Qy        638 CPYL 641
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Db        679 CPYL 682

RESULT 11
US-10-399-443-2
; Sequence 2, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute
;  APPLICANT:  Health
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
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;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 385
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-399-443-2

  Query Match            11.8%;  Score 158;  DB 15;  Length 385;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-142;
  Matches  158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        290 AEKQPPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLL 349
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         39 AEKQPPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLL 98

Qy        350 LERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGL 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 LERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGL 158

Qy        410 HAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGV 447
              |||||||||||||||||||||||||||||||||||||
Db        159 HAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGV 196


RESULT 12
US-10-677-943-2
; Sequence 2, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 385
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-677-943-2

  Query Match            11.8%;  Score 158;  DB 15;  Length 385;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-142;
  Matches  158;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        290 AEKQPPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLL 349
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Db         39 AEKQPPPFTLIRSLLRKVLLPESFLIVTVRDVGTEKLKSEVVSPRYLLVRGISGEQRIHLL 98

Qy        350 LERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGL 409
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 LERGIGEHQKTQGLRAIMNNRELLDQCQVPAVGSLICVALQLQDVVGESVAPFNQTLTGL 158

Qy        410 HAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGV 447
              |||||||||||||||||||||||||||||||||||||
Db        159 HAAFVFHQLTPRGVVRRCLNLEERVVLKRFCRMAVEGV 196


RESULT 13
US-10-399-443-4
; Sequence 4, Application US/10399443
; Publication No. US20040028669A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America, as Represented by the
;  APPLICANT:  Secretary, Department of Health & Human Services, The National Institute
;  APPLICANT:  Health
;  APPLICANT:  Nelson, Lawrence M.
;  APPLICANT:  Tong, Zhi-Bin
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Zhi-Bin, Tong
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64785
;  CURRENT APPLICATION NUMBER: US/10/399,443
;  CURRENT FILING DATE:  2003-04-16
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-399-443-4

  Query Match            11.1%;  Score 149;  DB 15;  Length 258;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-134;
  Matches  149;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        918 LTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKS 977
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 LTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKS 127

Qy        978 LDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNL 1037
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 LDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNL 187

Qy       1038 VQNNFSPKGMMKLCSAFACPTSNLQIIGL 1066
              |||||||||||||||||||||||||||||
Db        188 VQNNFSPKGMMKLCSAFACPTSNLQIIGL 216


RESULT 14
US-10-677-943-4
; Sequence 4, Application US/10677943
; Publication No. US20040072297A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as
;  APPLICANT:  represented by the Secretary of the Department of Health and
;  APPLICANT:  Human Services
;  APPLICANT:  Nelson, Lawrence
;  APPLICANT:  Tong, Zhi-Bin
;  TITLE OF INVENTION: Human Gene Critical to Fertility
;  FILE REFERENCE: 4239-64790
;  CURRENT APPLICATION NUMBER: US/10/677,943
;  CURRENT FILING DATE:  2003-10-01
;  PRIOR APPLICATION NUMBER: 60/241,510
;  PRIOR FILING DATE: 2000-10-18
;  PRIOR APPLICATION NUMBER: PCT/US02/09776
;  PRIOR FILING DATE: 2002-03-29
;  PRIOR APPLICATION NUMBER: PCT/US01/10981
;  PRIOR FILING DATE: 2001-04-04
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-677-943-4

  Query Match            11.1%;  Score 149;  DB 15;  Length 258;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-134;
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  Matches  149;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        918 LTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKS 977
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 LTHLSLSMNPVEDNGVKLLCEVMREPSCHLQDLELVKCHLTAACCESLSCVISRSRHLKS 127

Qy        978 LDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNL 1037
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 LDLTDNALGDGGVAALCEGLKQKNSVLTRLGLKACGLTSDCCEALSLALSCNRHLTSLNL 187

Qy       1038 VQNNFSPKGMMKLCSAFACPTSNLQIIGL 1066
              |||||||||||||||||||||||||||||
Db        188 VQNNFSPKGMMKLCSAFACPTSNLQIIGL 216


RESULT 15
US-09-965-621-63
; Sequence 63, Application US/09965621
; Publication No. US20030077699A1
; GENERAL INFORMATION:
;  APPLICANT: Reed, John C.
;  APPLICANT:  Godzik, Adam
;  APPLICANT:  Chu, Zhi-Liang
;  APPLICANT:  Pawlowski, Krzysztof
;  APPLICANT:  Fiorentino, Loredana
;  APPLICANT:  Ariza, Maria Eugenia
;  APPLICANT:  Stehlik, Christian
;  TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
;  TITLE OF INVENTION:  Encoding Nucleic Acids, and Methods of Use
;  FILE REFERENCE: P-LJ 4816
;  CURRENT APPLICATION NUMBER: US/09/965,621
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: US 09/671,760
;  PRIOR FILING DATE: 2000-09-26
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
;   LENGTH: 190
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-965-621-63

  Query Match             0.9%;  Score 12;  DB 10;  Length 190;
  Best Local Similarity   100.0%;  Pred. No. 0.019;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        262 PERLLFIIDGFD 273
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Db         77 PERLLFIIDGFD 88


Search completed: July 19, 2005, 12:27:33
Job time : 127 secs
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